



SEQUENCE LISTING

<110> Sheppard, Paul O.

<120> IL-28 AND IL-29 TRUNCATED CYSTEINE  
MUTANTS AND METHODS OF USING SAME

<130> 05-22P1

<160> 150

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 618

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(618)

<221> misc\_feature

<222> (0)...(0)

<223> IL-28A

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acc gtg act gga gca gtt cct gtc gcc agg ctc cac ggg gct ctc ccg	96
Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His Gly Ala Leu Pro	30
20 25	
gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct cca cag	144
Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln	45
35 40	
gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag tgc ctt	192
Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu	60
50 55	
ctg ctg aag gac tgc agg tgc cac tcc cgc ctc ttc ccc agg acc tgg	240
Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp	80
65 70 75	
gac ctg agg cag ctg cag gtg agg gag cgc ccc atg gct ttg gag gct	288
Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala	95
85 90	
gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac act gac	336
Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp	110
100 105	
cca gcc ctg gtg gac gtc ttg gac cag ccc ctt cac acc ctg cac cat	384
Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His Thr Leu His His	125
115 120	
atc ctc tcc cag ttc cgg gcc tgt gtg agt cgt cag ggc ctg ggc acc	432
Ile Leu Ser Gln Phe Arg Ala Cys Val Ser Arg Gln Gly Leu Gly Thr	140
130 135	
cag atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc cgc ctc	480

Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu  
 145 150 155 160  
 cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag gag tcc cct 528  
 His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro  
 165 170 175  
 ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 576  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 180 185 190  
 cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc tga 618  
 Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val \*  
 195 200 205

<210> 2  
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 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu  
 50 55 60  
 Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp  
 65 70 75 80  
 Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala  
 85 90 95  
 Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp  
 100 105 110  
 Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His Thr Leu His His  
 115 120 125  
 Ile Leu Ser Gln Phe Arg Ala Cys Val Ser Arg Gln Gly Leu Gly Thr  
 130 135 140  
 Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu  
 145 150 155 160  
 His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro  
 165 170 175  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 180 185 190  
 Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
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<210> 3  
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<220>  
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 <222> (1)...(603)  
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 <222> (0)...(0)  
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gcc gtg gca ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag 96  
 Ala Val Ala Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys 30  
 20 25

ggc tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg 144  
 Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala 45  
 35 40

agc ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa 192  
 Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys 60  
 50 55

aac tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg 240  
 Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg 80  
 65 70 75

ctt ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc 288  
 Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala 95  
 85 90

ctg acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac 336  
 Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp 110  
 100 105

gtc cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc 384  
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu 125  
 115 120

cag gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg gcc 432  
 Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly 140  
 130 135

cgc ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag 480  
 Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu 160  
 145 150 155

tcc gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc 528  
 Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu 175  
 165 170

ctc acg cga gac ctc aaa tat gtg gcc gat ggg gac ctg tgt ctg aga 576  
 Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg 190  
 180 185

acg tca acc cac cct gag tcc acc tga 603  
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 195 200

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 <211> 200  
 <212> PRT  
 <213> Homo sapiens

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 20 25  
 Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala 45  
 35 40

Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys  
 50 55 60  
 Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg  
 65 70 75 80  
 Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala  
 85 90 95  
 Leu Thr Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp  
 100 105 110  
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu  
 115 120 125  
 Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly  
 130 135 140  
 Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu  
 145 150 155 160  
 Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu  
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 Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg  
 180 185 190  
 Thr Ser Thr His Pro Glu Ser Thr  
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 acc gtg act gga gca gtt cct gtc gcc agg ctg cgc ggg gct ctg ccg 96  
 Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro  
 20 25 30  
 gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct cca cag 144  
 Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln  
 35 40 45  
 gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt 192  
 Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu  
 50 55 60  
 ctg ctg aag gac tgc aag tgc cgc tcc cgc ctg ttc ccc agg acc tgg 240  
 Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp  
 65 70 75 80  
 gac ctg agg cag ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct 288  
 Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala  
 85 90 95  
 gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac act gac 336  
 Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp  
 100 105 110  
 cca gcc ctg ggg gat gtc ttg gac cag ccc ctt cac acc ctg cac cat 384



Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His Thr Leu His His  
 115 120 125

atc ctc tcc cag ctc cgg gcc tgt gtg agt cgt cag ggc ccg ggc acc 432  
 Ile Leu Ser Gln Leu Arg Ala Cys Val Ser Arg Gln Gly Pro Gly Thr  
 130 135 140

cag atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc cgc ctc 480  
 Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu  
 145 150 155 160

cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag gag tcc cct 528  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro  
 165 170 175

ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 576  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 180 185 190

cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc 615  
 Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 195 200 205

<210> 6  
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 35 40 45  
 Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu  
 50 55 60  
 Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp  
 65 70 75 80  
 Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala  
 85 90 95  
 Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp  
 100 105 110  
 Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His Thr Leu His His  
 115 120 125  
 Ile Leu Ser Gln Leu Arg Ala Cys Val Ser Arg Gln Gly Pro Gly Thr  
 130 135 140  
 Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu  
 145 150 155 160  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro  
 165 170 175  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
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 195 200 205

<210> 7  
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 <212> DNA  
 <213> Mus musculus

<220>  
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&lt;400&gt; 7

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ctc ctc ctg ctg ttg cct ctg ctg ctg gcc gca gtg ctg aca aga acc      99
Leu Leu Leu Leu Leu Pro Leu Leu Leu Ala Ala Val Leu Thr Arg Thr
                        15          20          25

caa gct gac cct gtc ccc agg gcc acc agg ctc cca gtg gaa gca aag      147
Gln Ala Asp Pro Val Pro Arg Ala Thr Arg Leu Pro Val Glu Ala Lys
                        30          35          40

gat tgc cac att gct cag ttc aag tct ctg tcc cca aaa gag ctg cag      195
Asp Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln
                        45          50          55

gcc ttc aaa aag gcc aag gat gcc atc gag aag agg ctg ctt gag aag      243
Ala Phe Lys Lys Ala Lys Asp Ala Ile Glu Lys Arg Leu Leu Glu Lys
                        60          65          70

gac ctg agg tgc agt tcc cac ctc ttc ccc agg gcc tgg gac ctg aag      291
Asp Leu Arg Cys Ser Ser His Leu Phe Pro Arg Ala Trp Asp Leu Lys
                        75          80          85          90

cag ctg cag gtc caa gag cgc ccc aag gcc ttg cag gct gag gtg gcc      339
Gln Leu Gln Val Gln Glu Arg Pro Lys Ala Leu Gln Ala Glu Val Ala
                        95          100          105

ctg acc ctg aag gtc tgg gag aac atg act gac tca gcc ctg gcc acc      387
Leu Thr Leu Lys Val Trp Glu Asn Met Thr Asp Ser Ala Leu Ala Thr
                        110          115          120

atc ctg ggc cag cct ctt cat aca ctg agc cac att cac tcc cag ctg      435
Ile Leu Gly Gln Pro Leu His Thr Leu Ser His Ile His Ser Gln Leu
                        125          130          135

cag acc tgt aca cag ctt cag gcc aca gca gag ccc agg tcc ccg agc      483
Gln Thr Cys Thr Gln Leu Gln Ala Thr Ala Glu Pro Arg Ser Pro Ser
                        140          145          150

cgc cgc ctc tcc cgc tgg ctg cac agg ctc cag gag gcc cag agc aag      531
Arg Arg Leu Ser Arg Trp Leu His Arg Leu Gln Glu Ala Gln Ser Lys
                        155          160          165          170

gag acc cct ggc tgc ctg gag gcc tct gtc acc tcc aac ctg ttt cgc      579
Glu Thr Pro Gly Cys Leu Glu Ala Ser Val Thr Ser Asn Leu Phe Arg
                        175          180          185

ctg ctc acc cgg gac ctc aag tgt gtg gcc aat gga gac cag tgt gtc      627
Leu Leu Thr Arg Asp Leu Lys Cys Val Ala Asn Gly Asp Gln Cys Val
                        190          195          200

tga cct
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633

&lt;210&gt; 8

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

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 Arg Ala Thr Arg Leu Pro Val Glu Ala Lys Asp Cys His Ile Ala Gln  
 35 40 45  
 Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln Ala Phe Lys Lys Ala Lys  
 50 55 60  
 Asp Ala Ile Glu Lys Arg Leu Leu Glu Lys Asp Leu Arg Cys Ser Ser  
 65 70 75 80  
 His Leu Phe Pro Arg Ala Trp Asp Leu Lys Gln Leu Gln Val Gln Glu  
 85 90 95  
 Arg Pro Lys Ala Leu Gln Ala Glu Val Ala Leu Thr Leu Lys Val Trp  
 100 105 110  
 Glu Asn Met Thr Asp Ser Ala Leu Ala Thr Ile Leu Gly Gln Pro Leu  
 115 120 125  
 His Thr Leu Ser His Ile His Ser Gln Leu Gln Thr Cys Thr Gln Leu  
 130 135 140  
 Gln Ala Thr Ala Glu Pro Arg Ser Pro Ser Arg Arg Leu Ser Arg Trp  
 145 150 155 160  
 Leu His Arg Leu Gln Glu Ala Gln Ser Lys Glu Thr Pro Gly Cys Leu  
 165 170 175  
 Glu Ala Ser Val Thr Ser Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu  
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 195 200

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 <212> DNA  
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<220>  
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 Leu Leu Leu Leu Leu Pro Leu Leu Leu Ala Ala Val Leu Thr Arg Thr 25  
 15 20  
 caa gct gac cct gtc ccc agg gcc acc agg ctc cca gtg gaa gca aag 147  
 Gln Ala Asp Pro Val Pro Arg Ala Thr Arg Leu Pro Val Glu Ala Lys 40  
 30 35  
 gat tgc cac att gct cag ttc aag tct ctg tcc cca aaa gag ctg cag 195  
 Asp Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln 55  
 45 50  
 gcc ttc aaa aag gcc aag ggt gcc atc gag aag agg ctg ctt gag aag 243  
 Ala Phe Lys Lys Ala Lys Gly Ala Ile Glu Lys Arg Leu Leu Glu Lys 70  
 60 65  
 gac atg agg tgc agt tcc cac ctc atc tcc agg gcc tgg gac ctg aag 291  
 Asp Met Arg Cys Ser Ser His Leu Ile Ser Arg Ala Trp Asp Leu Lys 90  
 75 80 85  
 cag ctg cag gtc caa gag cgc ccc aag gcc ttg cag gct gag gtg gcc 339  
 Gln Leu Gln Val Gln Glu Arg Pro Lys Ala Leu Gln Ala Glu Val Ala

95 100 105  
 ctg acc ctg aag gtc tgg gag aac ata aat gac tca gcc ctg acc acc 387  
 Leu Thr Leu Lys Val Trp Glu Asn Ile Asn Asp Ser Ala Leu Thr Thr  
 110 115 120  
 atc ctg ggc cag cct ctt cat aca ctg agc cac att cac tcc cag ctg 435  
 Ile Leu Gly Gln Pro Leu His Thr Leu Ser His Ile His Ser Gln Leu  
 125 130 135  
 cag acc tgt aca cag ctt cag gcc aca gca gag ccc aag ccc ccg agt 483  
 Gln Thr Cys Thr Gln Leu Gln Ala Thr Ala Glu Pro Lys Pro Pro Ser  
 140 145 150  
 cgc cgc ctc tcc cgc tgg ctg cac agg ctc cag gag gcc cag agc aag 531  
 Arg Arg Leu Ser Arg Trp Leu His Arg Leu Gln Glu Ala Gln Ser Lys  
 155 160 165 170  
 gag act cct ggc tgc ctg gag gac tct gtc acc tcc aac ctg ttt caa 579  
 Glu Thr Pro-Gly-Cys-Leu Glu Asp Ser Val Thr Ser Asn Leu Phe Gln  
 175 180 185  
 ctg ctc ctc cgg gac ctc aag tgt gtg gcc agt gga gac cag tgt gtc 627  
 Leu Leu Leu Arg Asp Leu Lys Cys Val Ala Ser Gly Asp Gln Cys Val  
 190 195 200  
 tga cc 632  
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<210> 10  
 <211> 202  
 <212> PRT  
 <213> Mus musculus

<400> 10  
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 20 25 30  
 Arg Ala Thr Arg Leu Pro Val Glu Ala Lys Asp Cys His Ile Ala Gln  
 35 40 45  
 Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln Ala Phe Lys Lys Ala Lys  
 50 55 60  
 Gly Ala Ile Glu Lys Arg Leu Leu Glu Lys Asp Met Arg Cys Ser Ser  
 65 70 75 80  
 His Leu Ile Ser Arg Ala Trp Asp Leu Lys Gln Leu Gln Val Gln Glu  
 85 90 95  
 Arg Pro Lys Ala Leu Gln Ala Glu Val Ala Leu Thr Leu Lys Val Trp  
 100 105 110  
 Glu Asn Ile Asn Asp Ser Ala Leu Thr Thr Ile Leu Gly Gln Pro Leu  
 115 120 125  
 His Thr Leu Ser His Ile His Ser Gln Leu Gln Thr Cys Thr Gln Leu  
 130 135 140  
 Gln Ala Thr Ala Glu Pro Lys Pro Pro Ser Arg Arg Leu Ser Arg Trp  
 145 150 155 160  
 Leu His Arg Leu Gln Glu Ala Gln Ser Lys Glu Thr Pro Gly Cys Leu  
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 1 5 10 15  
 gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg 96  
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu  
 20 25 30  
 ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc 144  
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly  
 35 40 45  
 aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc 192  
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr  
 50 55 60  
 cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg 240  
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu  
 65 70 75 80  
 cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc 288  
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe  
 85 90 95  
 aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg 336  
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val  
 100 105 110  
 gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct 384  
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro  
 115 120 125  
 gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg 432  
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr  
 130 135 140  
 tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag gtg 480  
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val  
 145 150 155 160  
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 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr  
 165 170 175  
 ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa 576  
 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu  
 180 185 190  
 cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa 624  
 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys  
 195 200 205

tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca gaa Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu 210 215 220	672
gcc aac tgg gct ttc ctg gtg ctg cca tcg ctt ctg ata ctg ctg tta Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu 225 230 235 240	720
gta att gcc gca ggg ggt gtg atc tgg aag acc ctc atg ggg aac ccc Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro 245 250 255	768
tgg ttt cag cgg gca aag atg cca cgg gcc ctg gac ttt tct gga cac Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp Phe Ser Gly His 260 265 270	816
aca cac cct gtg gca acc ttt cag ccc agc aga cca gag tcc gtg aat Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg Pro Glu Ser Val Asn 275 280 285	864
gac ttg ttc ctc tgt ccc caa aag gaa ctg acc aga ggg gtc agg ccg Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr Arg Gly Val Arg Pro 290 295 300	912
acg cct cga gtc agg gcc cca gcc acc caa cag aca aga tgg aag aag Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg Trp Lys Lys 305 310 315 320	960
gac ctt gca gag gac gaa gag gag gag gat gag gag gac aca gaa gat Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp Thr Glu Asp 325 330 335	1008
ggc gtc agc ttc cag ccc tac att gaa cca cct tct ttc ctg ggg caa Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly Gln 340 345 350	1056
gag cac cag gct cca ggg cac tcg gag gct ggt ggg gtg gac tca ggg Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser Gly 355 360 365	1104
agg ccc agg gct cct ctg gtc cca agc gaa ggc tcc tct gct tgg gat Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp Asp 370 375 380	1152
tct tca gac aga agc tgg gcc agc act gtg gac tcc tcc tgg gac agg Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp Arg 385 390 395 400	1200
gct ggg tcc tct ggc tat ttg gct gag aag ggg cca ggc caa ggg ccg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro 405 410 415	1248
ggt ggg gat ggg cac caa gaa tct ctc cca cca cct gaa ttc tcc aag Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser Lys 420 425 430	1296
gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc tcc tcc tgg Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp 435 440 445	1344
gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc cct ggg gga Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly 450 455 460	1392

ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa agc agc cct 1440  
 Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro  
 465 470 475 480  
 gag gag gaa gag gag gcg agg gaa tca gaa att gag gac agc gat gcg 1488  
 Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala  
 485 490 495  
 ggc agc tgg ggg gct gag agc acc cag agg acc gag gac agg ggc cgg 1536  
 Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg  
 500 505 510  
 aca ttg ggg cat tac atg gcc agg tga 1563  
 Thr Leu Gly His Tyr Met Ala Arg \*  
 515 520

<210> 12  
 <211> 520  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln  
 1 5 10 15  
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu  
 20 25 30  
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly  
 35 40 45  
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr  
 50 55 60  
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu  
 65 70 75 80  
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe  
 85 90 95  
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val  
 100 105 110  
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro  
 115 120 125  
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr  
 130 135 140  
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val  
 145 150 155 160  
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr  
 165 170 175  
 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu  
 180 185 190  
 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys  
 195 200 205  
 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu  
 210 215 220  
 Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu  
 225 230 235 240  
 Val Ile Ala Ala Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro  
 245 250 255  
 Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp Phe Ser Gly His  
 260 265 270  
 Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg Pro Glu Ser Val Asn  
 275 280 285  
 Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr Arg Gly Val Arg Pro  
 290 295 300  
 Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg Trp Lys Lys  
 305 310 315 320  
 Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp Thr Glu Asp  
 325 330 335

Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly Gln  
 340 345 350  
 Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser Gly  
 355 360 365  
 Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp Asp  
 370 375 380  
 Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp Arg  
 385 390 395 400  
 Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro  
 405 410 415  
 Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser Lys  
 420 425 430  
 Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp  
 435 440 445  
 Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly  
 450 455 460  
 Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro  
 465 470 475 480  
 Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala  
 485 490 495  
 Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg  
 500 505 510  
 Thr Leu Gly His Tyr Met Ala Arg  
 515 520

<210> 13  
 <211> 1476  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(1476)

<221> misc\_feature  
 <222> (0)...(0)  
 <223> IL-28RA splice variant

<400> 13  
 atg gcg ggg ccc gag cgc tgg ggc ccc ctg ctc ctg tgc ctg ctg cag 48  
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln  
 1 5 10 15  
 gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg 96  
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu  
 20 25 30  
 ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc 144  
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly  
 35 40 45  
 aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc 192  
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr  
 50 55 60  
 cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg 240  
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu  
 65 70 75 80  
 cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc 288  
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe  
 85 90 95  
 aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg 336



Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val	100	105	110	
gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct	115	120	125	384
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro				
gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg	130	135	140	432
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr				
tac cag ctg ccc ccc tgc atg ccc cca ctg ttt ctg aag tat gag gtg	145	150	155	480
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val				
gca ttt tgg ggg ggg ggg gcc gga acc aag acc cta ttt cca gtc act	165	170	175	528
Ala Phe Trp Gly Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr				
ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa	180	185	190	576
Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu				
cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa	195	200	205	624
His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys				
tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca gaa	210	215	220	672
Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu				
gcc aac tgg gct ttc ctg gtg ctg cca tcg ctt ctg ata ctg ctg tta	225	230	235	720
Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu				
gta att gcc gca ggg ggt gtg atc tgg aag acc ctc atg ggg aac ccc	245	250	255	768
Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro				
tgg ttt cag cgg gca aag atg cca cgg gcc ctg gaa ctg acc aga ggg	260	265	270	816
Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Glu Leu Thr Arg Gly				
gtc agg ccg acg cct cga gtc agg gcc cca gcc acc caa cag aca aga	275	280	285	864
Val Arg Pro Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg				
tgg aag aag gac ctt gca gag gac gaa gag gag gag gat gag gag gac	290	295	300	912
Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp				
aca gaa gat ggc gtc agc ttc cag ccc tac att gaa cca cct tct ttc	305	310	315	960
Thr Glu Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe				
ctg ggg caa gag cac cag gct cca ggg cac tcg gag gct ggt ggg gtg	325	330	335	1008
Leu Gly Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val				
gac tca ggg agg ccc agg gct cct ctg gtc cca agc gaa ggc tcc tct	340	345	350	1056
Asp Ser Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser				
gct tgg gat tct tca gac aga agc tgg gcc agc act gtg gac tcc tcc				1104
Ala Trp Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser				

355 360 365

1152  
 tgg gac agg gct ggg tcc tct ggc tat ttg gct gag aag ggg cca ggc  
 Trp Asp Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly  
 370 375 380

1200  
 caa ggg ccg ggt ggg gat ggg cac caa gaa tct ctc cca cca cct gaa  
 Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu  
 385 390 395 400

1248  
 ttc tcc aag gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc  
 Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu  
 405 410 415

1296  
 tcc tcc tgg gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc  
 Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val  
 420 425 430

1344  
 cct ggg gga ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa  
 Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu  
 435 440 445

1392  
 agc agc cct gag gag gaa gag gag gcg agg gaa tca gaa att gag gac  
 Ser Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp  
 450 455 460

1440  
 agc gat gcg ggc agc tgg ggg gct gag agc acc cag agg acc gag gac  
 Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp  
 465 470 475 480

1476  
 agg ggc cgg aca ttg ggg cat tac atg gcc agg tga  
 Arg Gly Arg Thr Leu Gly His Tyr Met Ala Arg \*  
 485 490

<210> 14  
 <211> 491  
 <212> PRT  
 <213> Homo sapiens

<400> 14  
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln  
 1 5 10 15  
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu  
 20 25 30  
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly  
 35 40 45  
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr  
 50 55 60  
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu  
 65 70 75 80  
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe  
 85 90 95  
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val  
 100 105 110  
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro  
 115 120 125  
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr  
 130 135 140  
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val  
 145 150 155 160  
 Ala Phe Trp Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr  
 165 170 175  
 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu  
 180 185 190

His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys  
 195 200 205  
 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu  
 210 215 220  
 Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu  
 225 230 235 240  
 Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro  
 245 250 255  
 Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Glu Leu Thr Arg Gly  
 260 265 270  
 Val Arg Pro Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg  
 275 280 285  
 Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp  
 290 295 300  
 Thr Glu Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe  
 305 310 315 320  
 Leu Gly Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val  
 325 330 335  
 Asp Ser Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser  
 340 345 350  
 Ala Trp Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser  
 355 360 365  
 Trp Asp Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly  
 370 375 380  
 Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu  
 385 390 395 400  
 Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu  
 405 410 415  
 Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val  
 420 425 430  
 Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu  
 435 440 445  
 Ser Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp  
 450 455 460  
 Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp  
 465 470 475 480  
 Arg Gly Arg Thr Leu Gly His Tyr Met Ala Arg  
 485 490

<210> 15  
 <211> 674  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(636)  
 <221> misc\_feature  
 <222> (0)...(0)  
 <223> IL-28RA soluble variant

<400> 15  
 atg gcg ggg ccc gag cgc tgg ggc ccc ctg ctc ctg tgc ctg ctg cag 48  
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln  
 1 5 10 15  
 gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg 96  
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu  
 20 25 30  
 ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc 144  
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly  
 35 40 45

aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc 192  
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr  
 50 55 60

cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg 240  
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu  
 65 70 75 80

cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc 288  
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe  
 85 90 95

aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg 336  
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val  
 100 105 110

gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct 384  
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro  
 115 120 125

gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg 432  
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr  
 130 135 140

tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag gtg 480  
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val  
 145 150 155 160

gca ttc tgg aag gag ggg gcc gga aac aag gtg gga agc tcc ttt cct 528  
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Val Gly Ser Ser Phe Pro  
 165 170 175

gcc ccc agg cta ggc ccg ctc ctc cac ccc ttc tta ctc agg ttc ttc 576  
 Ala Pro Arg Leu Gly Pro Leu Leu His Pro Phe Leu Leu Arg Phe Phe  
 180 185 190

tca ccc tcc cag cct gct cct gca ccc ctc ctc cag gaa gtc ttc cct 624  
 Ser Pro Ser Gln Pro Ala Pro Ala Pro Leu Leu Gln Glu Val Phe Pro  
 195 200 205

gta cac tcc tga cttctggcag tcagccctaa taaaatctga tcaaagta 674  
 Val His Ser \*  
 210

<210> 16  
 <211> 211  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln  
 1 5 10 15  
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu  
 20 25 30  
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly  
 35 40 45  
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr  
 50 55 60  
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu  
 65 70 75 80  
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe  
 85 90 95  
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val

100 105 110  
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro  
 115 120 125  
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr  
 130 135 140  
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val  
 145 150 155 160  
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Val Gly Ser Ser Phe Pro  
 165 170 175  
 Ala Pro Arg Leu Gly Pro Leu Leu His Pro Phe Leu Leu Arg Phe Phe  
 180 185 190  
 Ser Pro Ser Gln Pro Ala Pro Ala Pro Leu Leu Gln Glu Val Phe Pro  
 195 200 205  
 Val His Ser  
 210

<210> 17  
 <211> 734  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> (53)...(127)  
 <221> mat\_peptide  
 <222> (128)...(655)

<221> CDS  
 <222> (53)...(655)

<400> 17  
 tgggtgacag cctcagagtg tttcttctgc tgacaaagac cagagatcag ga atg aaa 58  
 Met Lys  
 -25

cta gac atg act ggg gac tgc acg cca gtg ctg gtg ctg atg gcc gca 106  
 Leu Asp Met Thr Gly Asp Cys Thr Pro Val Leu Val Leu Met Ala Ala  
 -20 -15 -10

gtg ctg acc gtg act gga gca gtt cct gtc gcc agg ctc cac ggg gct 154  
 Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His Gly Ala  
 -5 1 5

ctc ccg gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct 202  
 Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser  
 10 15 20 25

cca cag gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag 250  
 Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu  
 30 35 40

tcg ctt ctg ctg aag gac tgc agg tgc cac tcc cgc ctc ttc ccc agg 298  
 Ser Leu Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe Pro Arg  
 45 50 55

acc tgg gac ctg agg cag ctg cag gtg agg gag cgc ccc atg gct ttg 346  
 Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met Ala Leu  
 60 65 70

gag gct gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac 394  
 Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp  
 75 80 85

act gac cca gcc ctg gtg gac gtc ttg gac cag ccc ctt cac acc ctg 442  
 Thr Asp Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His Thr Leu 105  
 90 95 100

cac cat atc ctc tcc cag ttc cgg gcc tgt atc cag cct cag ccc acg 490  
 His His Ile Leu Ser Gln Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr 120  
 110 115

gca ggg ccc agg acc cgg ggc cgc ctc cac cat tgg ctg tac cgg ctc 538  
 Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu Tyr Arg Leu 135  
 125 130

cag gag gcc cca aaa aag gag tcc cct ggc tgc ctc gag gcc tct gtc 586  
 Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala Ser Val 150  
 140 145

acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctg aat tgt gtt gcc 634  
 Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys Val Ala 165  
 155 160

agt ggg gac ctg tgt gtc tga ccctcccacc agtcatgcaa cctgagattt 685  
 Ser Gly Asp Leu Cys Val \*  
 170 175

tatttataaaa ttagccactt gtcttaattt attgccaccc agtcgctat 734

<210> 18  
 <211> 200  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> (1)... (25)

<400> 18  
 Met Lys Leu Asp Met Thr Gly Asp Cys Thr Pro Val Leu Val Leu Met  
 -25 -20 -15 -10  
 Ala Ala Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His  
 -5 1 5  
 Gly Ala Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser  
 10 15 20  
 Leu Ser Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu  
 25 30 35  
 Glu Glu Ser Leu Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe  
 40 45 50 55  
 Pro Arg Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met  
 60 65 70  
 Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr  
 75 80 85  
 Ala Asp Thr Asp Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His  
 90 95 100  
 Thr Leu His His Ile Leu Ser Gln Phe Arg Ala Cys Ile Gln Pro Gln  
 105 110 115  
 Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu Tyr  
 120 125 130 135  
 Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala  
 140 145 150  
 Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys  
 155 160 165  
 Val Ala Ser Gly Asp Leu Cys Val  
 170 175

<210> 19

<211> 856  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> (98)...(154)

<221> mat\_peptide  
 <222> (155)...(700)

<221> CDS  
 <222> (98)...(700)

<400> 19  
 aattaccttt tcactttaca cacatcatct tggattgcc attttgctg gctaaaaagc 60  
 agagccatgc cgctggggaa gcagttgcga tttagcc atg gct gca gct tgg acc 115  
 Met Ala Ala Ala Trp Thr  
 -15

gtg gtg ctg gtg act ttg gtg cta ggc ttg gcc gtg gca ggc cct gtc 163  
 Val Val Leu Val Thr Leu Val Leu Gly Leu Ala Val Ala Gly Pro Val  
 -10 -5 1

ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg 211  
 Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg  
 5 10 15

ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg 259  
 Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg  
 20 25 30 35

gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct 307  
 Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser  
 40 45 50

cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag 355  
 Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu  
 55 60 65

cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg 403  
 Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu  
 70 75 80

gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt 451  
 Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu  
 85 90 95

cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct 499  
 His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro  
 100 105 110 115

cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg 547  
 Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu  
 120 125 130

cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag 595  
 His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu  
 135 140 145

gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa 643  
 Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys  
 150 155 160

tat gtg gcc gat ggg aac ctg tgt ctg aga acg tca acc cac cct gag 691

Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr His Pro Glu  
 165 170 175

740

tcc acc tga caccacac cttatttatg cgctgagccc tactccttcc  
 Ser Thr \*  
 180

ttaatttatt tcctctcacc ctttatttat gaagctgcag ccctgactga gacatagggc 800  
 tgagtttatt gttttacttt tatacattat gcacaaataa acaacaagga attgga 856

<210> 20  
 <211> 200  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> (1)...(19)

<400> 20  
 Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu  
 -15 -10 -5  
 Ala Val Ala Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys  
 1 5 10  
 Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala  
 15 20 25  
 Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys  
 30 35 40 45  
 Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg  
 50 55 60  
 Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala  
 65 70 75  
 Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp  
 80 85 90  
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu  
 95 100 105  
 Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly  
 110 115 120 125  
 Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu  
 130 135 140  
 Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu  
 145 150 155  
 Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg  
 160 165 170  
 Thr Ser Thr His Pro Glu Ser Thr  
 175 180

<210> 21  
 <211> 734  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> (53)...(127)

<221> mat\_peptide  
 <222> (128)...(655)

<221> CDS  
 <222> (53)...(655)

<400> 21  
 tgggtgacag cctcagagt tttcttctgc tgacaaagac cagagatcag ga atg aaa 58



Met Lys  
-25

cta gac atg acc ggg gac tgc atg cca gtg ctg gtg ctg atg gcc gca 106  
 Leu Asp Met Thr Gly Asp Cys Met Pro Val Leu Val Leu Met Ala Ala  
 -20 -15 -10

gtg ctg acc gtg act gga gca gtt cct gtc gcc agg ctc cgc ggg gct 154  
 Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg Gly Ala  
 -5 1 5

ctc ccg gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct 202  
 Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser  
 10 15 20 25

cca cag gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag 250  
 Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu  
 30 35 40

tcg ctt ctg ctg aag gac tgc aag tgc cgc tcc cgc ctc ttc ccc agg 298  
 Ser Leu Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg  
 45 50 55

acc tgg gac ctg agg cag ctg cag gtg agg gag cgc ccc gtg gct ttg 346  
 Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val Ala Leu  
 60 65 70

gag gct gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac 394  
 Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp  
 75 80 85

act gac cca gcc ctg ggg gat gtc ttg gac cag ccc ctt cac acc ctg 442  
 Thr Asp Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His Thr Leu  
 90 95 100 105

cac cat atc ctc tcc cag ctc cgg gcc tgt atc cag cct cag ccc acg 490  
 His His Ile Leu Ser Gln Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr  
 110 115 120

gca ggg ccc agg acc cgg ggc cgc ctc cac cat tgg ctg cac cgg ctc 538  
 Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu His Arg Leu  
 125 130 135

cag gag gcc cca aaa aag gag tcc cct ggc tgc ctc gag gcc tct gtc 586  
 Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala Ser Val  
 140 145 150

acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctg aat tgt gtt gcc 634  
 Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys Val Ala  
 155 160 165

agc ggg gac ctg tgt gtc tga cccttcgcc agtcatgcaa cctgagattt 685  
 Ser Gly Asp Leu Cys Val \*

tatttataaaa ttagccactt ggcttaattt attgccaccc agtcgctat 734

<210> 22  
 <211> 200  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> (1)...(25)

<400> 22  
 Met Lys Leu Asp Met Thr Gly Asp Cys Met Pro Val Leu Val Leu Met  
 -25 -20 -15 -10  
 Ala Ala Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg  
 -5 1 5  
 Gly Ala Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser  
 10 15 20  
 Leu Ser Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu  
 25 30 35  
 Glu Glu Ser Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe  
 40 45 50 55  
 Pro Arg Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val  
 60 65 70  
 Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr  
 75 80 85  
 Ala Asp Thr Asp Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His  
 90 95 100  
 Thr Leu His His Ile Leu Ser Gln Leu Arg Ala Cys Ile Gln Pro Gln  
 105 110 115  
 Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu His  
 120 125 130 135  
 Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala  
 140 145 150  
 Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys  
 155 160 165  
 Val Ala Ser Gly Asp Leu Cys Val  
 170 175

<210> 23  
 <211> 528  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IL-28A mutant C48S

<221> CDS  
 <222> (1)...(528)

<400> 23  
 gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc tgc 48  
 Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys  
 1 5 10 15  
 cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96  
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe  
 20 25 30  
 aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tcc 144  
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Ser  
 35 40 45  
 agg tgc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192  
 Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu  
 50 55 60  
 cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg acg 240  
 Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg gac 288  
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp  
 85 90 95

gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ttc 336  
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe  
 100 105 110

cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc 384  
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly  
 115 120 125

cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag gag 432  
 Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu  
 130 135 140

tcc cct gcc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc 480  
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu  
 145 150 155 160

ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc tga 528  
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val \*  
 165 170 175

<210> 24  
 <211> 175  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-28A mutant C48S

<400> 24  
 Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys  
 1 5 10 15  
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe  
 20 25 30  
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Ser  
 35 40 45  
 Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp  
 85 90 95  
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe  
 100 105 110  
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly  
 115 120 125  
 Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu  
 130 135 140  
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu  
 145 150 155 160  
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

<210> 25  
 <211> 531  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> met IL-28A mutant C49S

<221> CDS

&lt;222&gt; (1)...(531)

&lt;400&gt; 25

atg gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc	48
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly	
1 5 10 15	
tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc	96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala	
20 25 30	
ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac	144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp	
35 40 45	
tcc agg tgc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag	192
Ser Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln	
50 55 60	
ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg	240
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu	
65 70 75 80	
acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg	288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val	
85 90 95	
gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag	336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln	
100 105 110	
ttc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg	384
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg	
115 120 125	
ggc cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag	432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys	
130 135 140	
gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc	480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg	
145 150 155 160	
ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc	528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val	
165 170 175	
tga	531
*	

&lt;210&gt; 26

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; met IL-28A mutant C49S

&lt;400&gt; 26

Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly	
1 5 10 15	
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala	
20 25 30	

Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp  
                   35                  40                  45  
 Ser Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln  
           50                  55                  60  
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu  
 65                  70                  75                  80  
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val  
                   85                  90                  95  
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln  
                   100                  105                  110  
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg  
           115                  120                  125  
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys  
 130                  135                  140  
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg  
 145                  150                  155                  160  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
                   165                  170                  175

<210> 27  
 <211> 528  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IL-28A mutant C50S

<221> CDS  
 <222> (1)...(528)

<400> 27  
 gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc tgc 48  
 Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys  
   1                  5                  10                  15  
  
 cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96  
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe  
                   20                  25                  30  
  
 aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tgc 144  
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Cys  
                   35                  40                  45  
  
 agg tcc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192  
 Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu  
                   50                  55                  60  
  
 cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg acg 240  
 Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr  
                   65                  70                  75                  80  
  
 ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg gac 288  
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp  
                   85                  90                  95  
  
 gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ttc 336  
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe  
                   100                  105                  110  
  
 cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc 384  
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly  
                   115                  120                  125  
  
 cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag gag 432

Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu  
 130 135 140

tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc 480  
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu  
 145 150 155 160

ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc tga 528  
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val \*  
 165 170 175

<210> 28  
 <211> 175  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-28A mutant C50S

<400> 28  
 Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys  
 1 5 10 15  
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe  
 20 25 30  
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Cys  
 35 40 45  
 Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp  
 85 90 95  
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe  
 100 105 110  
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly  
 115 120 125  
 Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu  
 130 135 140  
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu  
 145 150 155 160  
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

<210> 29  
 <211> 531  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> met IL-28A mutant C51S

<221> CDS  
 <222> (1)...(531)

<400> 29  
 atg gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc 48  
 Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly  
 1 5 10 15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96  
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala  
 20 25 30

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ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
      35              40              45

tgc agg tcc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192
Cys Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
      50              55              60

ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg 240
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
      65              70              75              80

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg 288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
      85              90              95

gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
      100              105              110

ttc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg 384
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
      115              120              125

ggc cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag 432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
      130              135              140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
      145              150              155              160

ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc 528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
      165              170              175

tga 531
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<210> 30  
 <211> 176  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> met IL-28A mutant C51S

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<400> 30
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
1      5      10      15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20     25     30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
35     40     45
Cys Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50     55     60
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
65     70     75     80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
85     90     95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100    105    110
```

Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg  
 115 120 125  
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys  
 130 135 140  
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg  
 145 150 155 160  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

<210> 31  
 <211> 546  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IL-29 mutant C171S

<221> CDS  
 <222> (1) (546)

<400> 31  
 ggt ccg gtt ccg acc tct aaa cca acc acc act ggt aaa ggt tgc cac 48  
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His  
 1 5 10 15  
 atc ggt cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc aaa 96  
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys  
 20 25 30  
 aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg tct 144  
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser  
 35 40 45  
 tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg cag 192  
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln  
 50 55 60  
 gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc ctg 240  
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu  
 65 70 75 80  
 aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg gat 288  
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp  
 85 90 95  
 cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct tgc 336  
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys  
 100 105 110  
 att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg cac 384  
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His  
 115 120 125  
 cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct ggt 432  
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly  
 130 135 140  
 tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc cgt 480  
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
 145 150 155 160  
 gat ctg aaa tac gtt gct gat ggt aac ctg tct ctg cgt acc tct acc 528  
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser Thr  
 165 170 175



cat ccg gaa tct acc taa  
His Pro Glu Ser Thr \*  
180

<210> 32  
<211> 181  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> IL-29 mutant C171S

<400> 32  
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His  
1 5 10 15  
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys  
20 25 30  
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser  
35 40 45  
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln  
50 55 60  
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu  
65 70 75 80  
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp  
85 90 95  
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys  
100 105 110  
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His  
115 120 125  
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly  
130 135 140  
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
145 150 155 160  
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser Thr  
165 170 175  
His Pro Glu Ser Thr  
180

<210> 33  
<211> 549  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> met IL-29 mutant C172S

<221> CDS  
<222> (1)...(549)

<400> 33  
atg ggt ccg gtt ccg acc tct aaa cca acc acc act ggt aaa ggt tgc 48  
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys  
1 5 10 15  
cac atc ggt cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc 96  
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
20 25 30  
aaa aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg 144  
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
35 40 45

tct tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg 192  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc 240  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 ctg aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg 288  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 gat cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct 336  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 tgc att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg 384  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 cac cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct 432  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc 480  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 cgt gat ctg aaa tac gtt gct gat ggt aac ctg tct ctg cgt acc tct 528  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser  
 165 170 175  
 acc cat ccg gaa tct acc taa 549  
 Thr His Pro Glu Ser Thr \*  
 180

<210> 34  
 <211> 182  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> met IL-29 mutant C172S

<400> 34  
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys  
 1 5 10 15  
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr

```
<221> CDS
<222> (1) ... (531)
```

[illegible]

<210> 36  
 <211> 176  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> met IL-28A

<400> 36  
 Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly  
 1 5 10 15  
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala  
 20 25 30  
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp  
 35 40 45  
 Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln  
 50 55 60  
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu  
 65 70 75 80  
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val  
 85 90 95  
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln  
 100 105 110  
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg  
 115 120 125  
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys  
 130 135 140  
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg  
 145 150 155 160  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

<210> 37  
 <211> 621  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> met IL-29  
 <221> CDS  
 <222> (1)...(549)

<400> 37  
 atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc 48  
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys  
 1 5 10 15  
 cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96  
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144  
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240

Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg aac ctg tgt ctg aga acg tca 528  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser  
 165 170 175

acc cac cct gag tcc acc tga caccacac cttatttatg cgctgagccc 579  
 Thr His Pro Glu Ser Thr \*  
 180

tactccttcc-ttaatttatt tcctctcacc-ctttatttat ga 621

<210> 38

<211> 182

<212> PRT

<213> Artificial Sequence

<220>

<223> met IL-29

<400> 38

Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys  
 1 5 10 15  
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser  
 165 170 175  
 Thr His Pro Glu Ser Thr

180

<210> 39  
 <211> 531  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> met IL-28B

<221> CDS  
 <222> (1) ... (531)

<400> 39  
 atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc 48  
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly  
 1 5 10 15

---

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96  
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala  
 20 25 30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144  
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp  
 35 40 45

tgc aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192  
 Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln  
 50 55 60

ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg 240  
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu  
 65 70 75 80

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg 288  
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly  
 85 90 95

gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336  
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln  
 100 105 110

ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg 384  
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg  
 115 120 125

ggc cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag 432  
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys  
 130 135 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480  
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg  
 145 150 155 160

ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc 528  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

tga 531  
 \*

<210> 40

<211> 176  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> met IL-28B

<400> 40  
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly  
 1 5 10 15  
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala  
 20 25 30  
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp  
 35 40 45  
 Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln  
 50 55 60  
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu  
 65 70 75 80  
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly  
 85 90 95  
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln  
 100 105 110  
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg  
 115 120 125  
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys  
 130 135 140  
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg  
 145 150 155 160  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

<210> 41  
 <211> 546  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IL-29 Cys15 mutant, Asn169

<221> CDS  
 <222> (1)...(546)

<221> variation  
 <222> (44)...(45)  
 <223> n = A, T, G, or C

<400> 41  
 ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn cac 48  
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His  
 1 5 10 15  
 att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96  
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys  
 20 25 30  
 aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144  
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser  
 35 40 45  
 tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192  
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln  
 50 55 60  
 gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240

Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu  
 65 70 75 80  
 aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac 288  
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp  
 85 90 95  
 cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336  
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys  
 100 105 110  
 atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384  
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His  
 115 120 125  
 cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc 432  
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly  
 130 135 140  
 tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480  
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
 145 150 155 160  
 gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca acc 528  
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr  
 165 170 175  
 cac cct gag tcc acc tga 546  
 His Pro Glu Ser Thr \*  
 180

&lt;210&gt; 42

&lt;211&gt; 181

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; IL-29 Cys15 mutant, Asn169

&lt;221&gt; VARIANT

&lt;222&gt; (15)...(15)

&lt;223&gt; Xaa = Ser, Ala, Thr, Val, or Asn

&lt;400&gt; 42

Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His  
 1 5 10 15  
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys  
 20 25 30  
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser  
 35 40 45  
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln  
 50 55 60  
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu  
 65 70 75 80  
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp  
 85 90 95  
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys  
 100 105 110  
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His  
 115 120 125  
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly  
 130 135 140  
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
 145 150 155 160



Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr  
 165 170 175  
 His Pro Glu Ser Thr  
 180

<210> 43  
 <211> 549  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Met IL-29 Cys16 mutant, Asn170

<221> CDS  
 <222> (1)...(549)

<221> variation  
 <222> (47)...(48)  
 <223> n = A, T, G, or C

<400> 43  
 atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn 48  
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa  
 1 5 10 15  
 cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96  
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144  
 Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 cga gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca 528  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser  
 165 170 175

acc cac cct gag tcc acc tga  
 Thr His Pro Glu Ser Thr \*  
 180

<210> 44  
 <211> 182  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Met IL-29 Cys16 mutant, Asn170

<221> VARIANT  
 <222> (16)...(16)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 44  
 Met Gly-Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa  
 1 5 10 15  
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser  
 165 170 175  
 Thr His Pro Glu Ser Thr  
 180

<210> 45  
 <211> 546  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IL-29 Cys15 mutant, Asp169

<221> CDS  
 <222> (1)...(546)

<221> variation  
 <222> (44)...(45)  
 <223> n = A, T, G, or C

<400> 45  
 ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn cac 48  
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His  
 1 5 10 15

```

att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag      96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
                20                25                30

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt      144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
                35                40                45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag      192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
                50                55                60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg      240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
                65                70                75                80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac      288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                85                90                95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt      336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
                100                105                110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac      384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
                115                120                125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc      432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
                130                135                140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga      480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
                145                150                155                160

gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca acc      528
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr
                165                170                175

cac cct gag tcc acc tga
His Pro Glu Ser Thr *
                180

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&lt;210&gt; 46

&lt;211&gt; 181

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; IL-29 Cys15 mutant, Asp169

&lt;221&gt; VARIANT

&lt;222&gt; (15)...(15)

&lt;223&gt; Xaa = Ser, Ala, Thr, Val, or Asn

&lt;400&gt; 46

```

Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His
 1                5                10                15
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
                20                25                30
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
                35                40                45
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln

```

50	55	60
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu		
65	70	75
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp		80
	85	90
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys		95
	100	105
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His		110
	115	120
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly		125
	130	135
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg		140
145	150	155
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr		160
	165	170
His Pro Glu Ser Thr		175
	180	

&lt;210&gt; 47

&lt;211&gt; 549

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Met IL-29 Cys16 mutant, Asp170

&lt;221&gt; CDS

&lt;222&gt; (1)...(549)

&lt;221&gt; variation

&lt;222&gt; (47)...(48)

&lt;223&gt; n = A, T, G, or C

&lt;400&gt; 47

atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn	48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa	
1 5 10 15	

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc	96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe	
20 25 30	

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg	144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp	
35 40 45	

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc	192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu	
50 55 60	

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg	240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr	
65 70 75 80	

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta	288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu	
85 90 95	

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc	336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala	
100 105 110	

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc	384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu	

115	120	125	
cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct			432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala			
130	135	140	
ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg			480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr			
145	150	155	160
cga gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca			528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser			
165	170	175	
acc cac cct gag tcc acc tga			549
Thr His Pro Glu Ser Thr *			
180			

<210> 48  
 <211> 182  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Met IL-29 Cys16 mutant,, Asp170  
  
 <221> VARIANT  
 <222> (16)...(16)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 48	
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa	
1	15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe	
20	30
Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp	
35	45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu	
50	60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr	
65	75
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu	
85	95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala	
100	110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu	
115	125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala	
130	140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr	
145	155
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser	
165	175
Thr His Pro Glu Ser Thr	
180	

<210> 49  
 <211> 546  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> IL-29 Asp169 Cys171 mutant

&lt;221&gt; CDS

&lt;222&gt; (1)...(546)

&lt;221&gt; variation.

&lt;222&gt; (512)...(513)

&lt;223&gt; n = A, T, G, or C

&lt;400&gt; 49

```

ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac 48
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
1           5           10           15

```

```

att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
           20           25           30

```

```

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
           35           40           45

```

```

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
           50           55           60

```

```

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65           70           75           80

```

```

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac 288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
           85           90           95

```

```

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
           100           105           110

```

```

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
           115           120           125

```

```

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc 432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
           130           135           140

```

```

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145           150           155           160

```

```

gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca acc 528
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr
           165           170           175

```

```

cac cct gag tcc acc tga 546
His Pro Glu Ser Thr *
           180

```

&lt;210&gt; 50

&lt;211&gt; 181

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; IL-29 Asp169 Cys171 mutant

<221> VARIANT

<222> (171)...(171)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 50

Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	Lys	Gly	Cys	His
1				5					10					15	
Ile	Gly	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	Ser	Phe	Lys
			20					25					30		
Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	Asn	Trp	Ser
		35					40					45			
Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu	Gln
	50				55					60					
Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Leu	Thr	Leu
65					70				75					80	
Lys	Val	Leu	Glu	Ala	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp	Val	Leu	Asp
			85					90					95		
Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu	Gln	Ala	Cys
		100						105					110		
Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly	Arg	Leu	His
		115					120					125			
His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	Ser	Ala	Gly
	130					135					140				
Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu	Leu	Thr	Arg
145					150					155					160
Asp	Leu	Lys	Tyr	Val	Ala	Asp	Gly	Asp	Leu	Xaa	Leu	Arg	Thr	Ser	Thr
			165					170						175	
His	Pro	Glu	Ser	Thr											
			180												

<210> 51

<211> 549

<212> DNA

<213> Artificial Sequence

<220>

<223> Met IL-29 Asp170 Cys172 mutant

<221> CDS

<222> (1)...(549)

<221> variation

<222> (515)...(516)

<223> n = A, T, G, or C

<400> 51

atg	ggc	cct	gtc	ccc	act	tcc	aag	ccc	acc	aca	act	ggg	aag	ggc	tgc	48
Met	Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	Lys	Gly	Cys	
1			5						10					15		
cac	att	ggc	agg	ttc	aaa	tct	ctg	tca	cca	cag	gag	cta	gcg	agc	ttc	96
His	Ile	Gly	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	Ser	Phe	
			20					25					30			
aag	aag	gcc	agg	gac	gcc	ttg	gaa	gag	tca	ctc	aag	ctg	aaa	aac	tgg	144
Lys	Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	Asn	Trp	
		35				40					45					
agt	tgc	agc	tct	cct	gtc	ttc	ccc	ggg	aat	tgg	gac	ctg	agg	ctt	ctc	192
Ser	Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu	
	50					55				60						
cag	gtg	agg	gag	cgc	cct	gtg	gcc	ttg	gag	gct	gag	ctg	gcc	ctg	acg	240

Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala 110  
 100 105

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu 125  
 115 120

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala 140  
 130 135

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr 160  
 145 150 155

cga gac ctc aaa tat gtg gcc gat ggg gag ctg dnn ctg aga acg tca 528  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser 175  
 165 170

acc cac cct gag tcc acc tga 549  
 Thr His Pro Glu Ser Thr \*

<210> 52

<211> 182

<212> PRT

<213> Artificial Sequence

<220>

<223> Met IL-29 Asp170 Cys172 mutant

<221> VARIANT

<222> (172)...(172)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 52

Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys  
 1 5 10 15  
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 His His Trp Leu His Arg Leu Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160



Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser  
 165 170 175  
 Thr His Pro Glu Ser Thr  
 180

<210> 53  
 <211> 546  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IL-29 Pro10 Asn169 Cys171 mutant

<221> CDS  
 <222> (1)...(546)

<221> variation  
 <222> (30)...(30)  
 <223> n = A, T, G, or C

<221> variation  
 <222> (512)...(513)  
 <223> n = A, T, G, or C

<400> 53  
 ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc tgc cac 48  
 Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys His  
 1 5 10 15  
 att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96  
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys  
 20 25 30  
 aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144  
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser  
 35 40 45  
 tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192  
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln  
 50 55 60  
 gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240  
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu  
 65 70 75 80  
 aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac 288  
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp  
 85 90 95  
 cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336  
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys  
 100 105 110  
 atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384  
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His  
 115 120 125  
 cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc 432  
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly  
 130 135 140  
 tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480  
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
 145 150 155 160

gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc 528  
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr  
                   165                  170                  175

cac cct gag tcc acc tga 546  
 His Pro Glu Ser Thr \*  
                   180

<210> 54  
 <211> 181  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-29 Pro10 Asn169 Cys171 mutant

<221> VARIANT  
 <222> (171)... (171)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 54  
 Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys His  
   1                  5                  10                  15  
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys  
                   20                  25                  30  
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser  
                   35                  40                  45  
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln  
                   50                  55                  60  
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu  
   65                  70                  75                  80  
 Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp  
                   85                  90                  95  
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys  
                   100                  105                  110  
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His  
                   115                  120                  125  
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly  
                   130                  135                  140  
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
   145                  150                  155                  160  
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr  
                   165                  170                  175  
 His Pro Glu Ser Thr  
                   180

<210> 55  
 <211> 549  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Met IL-29 Pro11 Asn170 Cys172 mutant

<221> CDS  
 <222> (1)... (549)

<221> variation  
 <222> 33, 515, 516  
 <223> n = A, T, G, or C

<400> 55

atg ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc tgc 48  
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys  
 1 5 10 15  
 cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96  
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144  
 Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca 528  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser  
 165 170 175  
 acc cac cct gag tcc acc tga 549  
 Thr His Pro Glu Ser Thr \*  
 180

&lt;210&gt; 56

&lt;211&gt; 182

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Met .IL-29 Pro11 Asn170 Cys172 mutant

&lt;221&gt; VARIANT

&lt;222&gt; (172)...(172)

&lt;223&gt; Xaa = Ser, Ala, Thr, Val, or Asn

&lt;400&gt; 56

Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys  
 1 5 10 15  
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe

20 25 30  
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser  
 165 170 175  
 Thr His Pro Glu Ser Thr  
 180

<210> 57  
 <211> 546  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IL-29 Pro10 Cys15 mutant Asn169

<221> CDS  
 <222> (1)...(546)

<221> variation  
 <222> (30)...(30)  
 <223> n = A, T, G, or C

<221> variation  
 <222> (44)...(45)  
 <223> n = A, T, G, or C

<400> 57  
 ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc dnn cac 48  
 Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa His  
 1 5 10 15

att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96  
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys  
 20 25 30

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144  
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser  
 35 40 45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192  
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln  
 50 55 60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240  
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu  
 65 70 75 80

aag gtc ctg gag gcc gct gct gcc cca gcc ctg gag gac gtc cta gac 288  
 Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp

85

90

95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336  
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys  
 100 105 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384  
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His  
 115 120 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc 432  
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly  
 130 135 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480  
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
 145 150 155 160

gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca acc 528  
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr  
 165 170 175

cac cct gag tcc acc tga 546  
 His Pro Glu Ser Thr \*

&lt;210&gt; 58

&lt;211&gt; 181

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; IL-29 Pro10 Cys15 mutant Asn169

&lt;221&gt; VARIANT

&lt;222&gt; (15)...(15)

&lt;223&gt; Xaa = Ser, Ala, Thr, Val, or Asn

&lt;400&gt; 58

Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa His  
 1 5 10 15  
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys  
 20 25 30  
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser  
 35 40 45  
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln  
 50 55 60  
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu  
 65 70 75 80  
 Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp  
 85 90 95  
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys  
 100 105 110  
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His  
 115 120 125  
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly  
 130 135 140  
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
 145 150 155 160  
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr  
 165 170 175  
 His Pro Glu Ser Thr  
 180

<210> 59  
 <211> 549  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Met IL-29 Pro11 Cys16 mutant Asn170

<221> CDS  
 <222> (1)...(549)

<221> variation  
 <222> (33)...(33)  
 <223> n = A, T, G, or C

<221> variation  
 <222> (47)...(48)  
 <223> n = A, T, G, or C

<400> 59  
 atg ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc dnn 48  
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa  
 1 5 10 15  
 cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96  
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144  
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 cga gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca 528  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser  
 165 170 175

acc cac cct gag tcc acc tga  
 Thr His Pro Glu Ser Thr \*  
 180

<210> 60  
 <211> 182  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Met\_IL-29\_Pro11 Cys16 mutant Asn170

<221> VARIANT  
 <222> (16)...(16)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 60  
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa  
 1 5 10 15  
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser  
 165 170 175  
 Thr His Pro Glu Ser Thr  
 180

<210> 61  
 <211> 546  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IL-29\_Pro10 Asp169 Cys171 mutant

<221> CDS  
 <222> (1)...(546)

<221> variation  
 <222> (30)...(30)  
 <223> n = A, T, G, or C

<221> variation  
 <222> (512)...(513)  
 <223> n = A, T, G, or C

<400> 61  
 ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc tgc cac 48

Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Pro	Thr	Gly	Lys	Gly	Cys	His	
1				5					10					15		
att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag	96															
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys																
20 25 30																
aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt	144															
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser																
35 40 45																
tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag	192															
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln																
50 55 60																
gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg	240															
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu																
65 70 75 80																
aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac	288															
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp																
85 90 95																
cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt	336															
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys																
100 105 110																
atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac	384															
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His																
115 120 125																
cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc	432															
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly																
130 135 140																
tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga	480															
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg																
145 150 155 160																
gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca acc	528															
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr																
165 170 175																
cac cct gag tcc acc tga	546															
His Pro Glu Ser Thr *																
180																

&lt;210&gt; 62

&lt;211&gt; 181

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; IL-29 Pro10 Asp169 Cys171 mutant

&lt;221&gt; VARIANT

&lt;222&gt; (171)...(171)

&lt;223&gt; Xaa = Ser, Ala, Thr, Val, or Asn

&lt;400&gt; 62

Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Pro	Thr	Gly	Lys	Gly	Cys	His	
1				5					10					15		
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys																
20 25 30																



Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser  
 35 40 45  
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln  
 50 55 60  
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu  
 65 70 75 80  
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp  
 85 90 95  
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys  
 100 105 110  
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His  
 115 120 125  
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly  
 130 135 140  
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
 145 150 155 160  
 Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr  
 165 170 175  
 His Pro Glu Ser Thr  
 180

<210> 63  
 <211> 549  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Met IL-29 Pro11 Asp170 Cys172 mutant

<221> CDS  
 <222> (1)...(549)

<221> variation  
 <222> (33)...(33)  
 <223> n = A, T, G, or C

<221> variation  
 <222> (515)...(516)  
 <223> n = A, T, G, or C

<400> 63  
 atg ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc tgc 48  
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys  
 1 5 10 15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96  
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144  
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336  
 Asp Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca 528  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser  
 165 170 175

acc cac cct gag tcc acc tga 549  
 Thr His Pro Glu Ser Thr \*  
 180

<210> 64

<211> 182

<212> PRT

<213> Artificial Sequence

<220>

<223> Met IL-29 Pro11 Asp170 Cys172 mutant

<221> VARIANT

<222> (172) ... (172)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 64

Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys  
 1 5 10 15  
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser  
 165 170 175  
 Thr His Pro Glu Ser Thr  
 180

<210> 65  
 <211> 546  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IL-29 Pro10 Cys15 mutant Asp169

<221> CDS  
 <222> (1)...(546)

<221> variation  
 <222> 30, 44, 45  
 <223> n = A, T, G, or C

<400> 65

ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc dnn cac	48
Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa His	
1 5 10 15	
att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag	96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys	
20 25 30	
aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt	144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser	
35 40 45	
tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag	192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln	
50 55 60	
gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg	240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu	
65 70 75 80	
aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac	288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp	
85 90 95	
cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt	336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys	
100 105 110	
atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac	384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His	
115 120 125	
cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc	432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly	
130 135 140	
tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga	480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg	
145 150 155 160	
gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca acc	528
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr	
165 170 175	
cac cct gag tcc acc tga	546
His Pro Glu Ser Thr *	
180	

<210> 66  
 <211> 181  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-29 Pro10 Cys15 mutant Asp169

<221> VARIANT  
 <222> (15)...(15)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 66  
 Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa His  
 1 5 10 15  
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys  
 20 25 30  
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser  
 35 40 45  
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln  
 50 55 60  
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Ala Leu Thr Leu  
 65 70 75 80  
 Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp  
 85 90 95  
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys  
 100 105 110  
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His  
 115 120 125  
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly  
 130 135 140  
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
 145 150 155 160  
 Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr  
 165 170 175  
 His Pro Glu Ser Thr  
 180

<210> 67  
 <211> 549  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Met IL-29 Pro11 Cys16 mutant Asp170

<221> CDS  
 <222> (1)...(549)

<221> variation  
 <222> 33, 47, 48  
 <223> n = A, T, G, or C

<400> 67  
 atg ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc dnn 48  
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa  
 1 5 10 15  
 cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96  
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144  
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp

35

40

45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca 528  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser  
 165 170 175

acc cac cct gag tcc acc tga 549  
 Thr His Pro Glu Ser Thr \*

&lt;210&gt; 68

&lt;211&gt; 182

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Met IL-29 Pro11 Cys16 mutant Asp170

&lt;221&gt; VARIANT

&lt;222&gt; (16)...(16)

&lt;223&gt; Xaa = Ser, Ala, Thr, Val, or Asn

&lt;400&gt; 68

Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa  
 1 5 10 15

His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30

Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45

Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60

Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80

Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95

Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala

	100		105		110										
Cys	Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly	Arg	Leu
	115						120					125			
His	His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	Ser	Ala
	130						135				140				
Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu	Leu	Thr
145					150					155					160
Arg	Asp	Leu	Lys	Tyr	Val	Ala	Asp	Gly	Asp	Leu	Cys	Leu	Arg	Thr	Ser
				165				170						175	
Thr	His	Pro	Glu	Ser	Thr										
			180												

&lt;210&gt; 69

&lt;211&gt; 546

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; IL-29 Asp18 Asn169 Cys171 mutant

&lt;221&gt; CDS

&lt;222&gt; (1)...(546)

&lt;221&gt; variation

&lt;222&gt; (512)...(513)

&lt;223&gt; n = A, T, G, or C

&lt;400&gt; 69

ggc	cct	gtc	ccc	act	tcc	aag	ccc	acc	aca	act	ggg	aag	ggc	tgc	cac	48
Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	Lys	Gly	Cys	His	
1				5						10				15		

att	gay	agg	ttc	aaa	tct	ctg	tca	cca	cag	gag	cta	gcg	agc	ttc	aag	96
Ile	Asp	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	Ser	Phe	Lys	
			20					25					30			

aag	gcc	agg	gac	gcc	ttg	gaa	gag	tca	ctc	aag	ctg	aaa	aac	tgg	agt	144
Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	Asn	Trp	Ser	
			35				40					45				

tgc	agc	tct	cct	gtc	ttc	ccc	ggg	aat	tgg	gac	ctg	agg	ctt	ctc	cag	192
Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu	Gln	
	50					55					60					

gtg	agg	gag	cgc	cct	gtg	gcc	ttg	gag	gct	gag	ctg	gcc	ctg	acg	ctg	240
Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Leu	Thr	Leu	
	65				70					75					80	

aag	gtc	ctg	gag	gcc	gct	gct	ggc	cca	gcc	ctg	gag	gac	gtc	cta	gac	288
Lys	Val	Leu	Glu	Ala	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp	Val	Leu	Asp	
				85					90					95		

cag	ccc	ctt	cac	acc	ctg	cac	cac	atc	ctc	tcc	cag	ctc	cag	gcc	tgt	336
Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu	Gln	Ala	Cys	
			100					105					110			

atc	cag	cct	cag	ccc	aca	gca	ggg	ccc	agg	ccc	cgg	ggc	cgc	ctc	cac	384
Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly	Arg	Leu	His	
			115				120					125				

cac	tgg	ctg	cac	cgg	ctc	cag	gag	gcc	ccc	aaa	aag	gag	tcc	gct	ggc	432
His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	Ser	Ala	Gly	
		130				135					140					

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480  
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
 145 150 155 160  
 gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc 528  
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr  
 165 170 175  
 cac cct gag tcc acc tga 546  
 His Pro Glu Ser Thr \*  
 180

<210> 70  
 <211> 181  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-29 Asp18 Asn169 Cys171 mutant

<221> VARIANT  
 <222> (171)...(171)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 70  
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His  
 1 5 10 15  
 Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys  
 20 25 30  
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser  
 35 40 45  
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln  
 50 55 60  
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu  
 65 70 75 80  
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp  
 85 90 95  
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys  
 100 105 110  
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His  
 115 120 125  
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly  
 130 135 140  
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
 145 150 155 160  
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr  
 165 170 175  
 His Pro Glu Ser Thr  
 180

<210> 71  
 <211> 549  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Met IL-29 Asp19 Asn170 Cys172 mutant

<221> CDS  
 <222> (1)...(549)  
 <221> variation  
 <222> (515)...(516)

<223> n = A, T, G, or C

<400> 71

atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc 48  
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys  
1 5 10 15

cac att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96  
His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
20 25 30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144  
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
35 40 45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192  
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
50 55 60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240  
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
65 70 75 80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288  
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336  
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384  
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
115 120 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432  
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480  
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca 528  
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser  
165 170 175

acc cac cct gag tcc acc tga 549  
Thr His Pro Glu Ser Thr \*

<210> 72

<211> 182

<212> PRT

<213> Artificial Sequence

<220>

<223> Met IL-29 Asp19 Asn170 Cys172 mutant

<221> VARIANT

<222> (172)...(172)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 72



Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys  
 1 5 10 15  
 His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser  
 165 170 175  
 Thr His Pro Glu Ser Thr  
 180

&lt;210&gt; 73

&lt;211&gt; 546

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; IL-29 Cys15 mutant Asp18 Asn169

&lt;221&gt; CDS

&lt;222&gt; (1)...(546)

&lt;221&gt; variation

&lt;222&gt; (44)...(45)

&lt;223&gt; n = A, T, G, or C

&lt;400&gt; 73

ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn cac 48  
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His 15  
 1 5 10

att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96  
 Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys 30  
 20 25

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144  
 Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp Ser 45  
 35 40

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192  
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln 60  
 50 55

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240  
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu 75 80  
 65 70

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac 288  
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp 95  
 85 90

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336  
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys  
 100 105 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384  
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His  
 115 120 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc 432  
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly  
 130 135 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480  
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
 145 150 155 160

gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca acc 528  
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr  
 165 170 175

cac cct gag tcc acc tga 546  
 His Pro Glu Ser Thr \*

<210> 74

<211> 181

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 Cys15 mutant Asp18 Asn169

<221> VARIANT

<222> (15).... (15)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 74

Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His  
 1 5 10 15  
 Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys  
 20 25 30  
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser  
 35 40 45  
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln  
 50 55 60  
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu  
 65 70 75 80  
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp  
 85 90 95  
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys  
 100 105 110  
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His  
 115 120 125  
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly  
 130 135 140  
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
 145 150 155 160  
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr  
 165 170 175  
 His Pro Glu Ser Thr  
 180

<210> 75  
 <211> 549  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Met IL-29 Cys16 mutant Asp19 Asn170

<221> CDS  
 <222> (1)...(549)

<221> variation  
 <222> (47)...(48)  
 <223> n = A, T, G, or C

<400> 75  
 atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn 48  
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa  
 1 5 10 15  
 cac att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96  
 His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144  
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 cga gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca 528  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser  
 165 170 175  
 acc cac cct gag tcc acc tga 549  
 Thr His Pro Glu Ser Thr \*  
 180

<210> 76  
 <211> 182  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Met IL-29 Cys16 mutant Asp19 Asn170

<221> VARIANT  
 <222> (16)...(16)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 76  
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa  
 1 5 10 15  
 His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser  
 165 170 175  
 Thr His Pro Glu Ser Thr  
 180

<210> 77  
 <211> 546  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IL-29 Asp18 Asp169 Cys171 mutant

<221> CDS  
 <222> (1)...(546)

<221> variation  
 <222> (512)...(513)  
 <223> n = A, T, G, or C

<400> 77  
 ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac 48  
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His  
 1 5 10 15  
 att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96  
 Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys  
 20 25 30  
 aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144  
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser

35

40

45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192  
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln  
 50 55 60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240  
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu  
 65 70 75 80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac 288  
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp  
 85 90 95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336  
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys  
 100 105 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384  
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His  
 115 120 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc 432  
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly  
 130 135 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480  
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
 145 150 155 160

gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca acc 528  
 Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr  
 165 170 175

cac cct gag tcc acc tga 546  
 His Pro Glu Ser Thr \*

<210> 78  
 <211> 181  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-29 Asp18 Asp169 Cys171 mutant

<221> VARIANT  
 <222> (171)...(171)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 78  
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His  
 1 5 10 15  
 Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys  
 20 25 30  
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser  
 35 40 45  
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln  
 50 55 60  
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu  
 65 70 75 80  
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp  
 85 90 95  
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys

	100		105		110								
Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Gly	Arg	Leu	His
	115						120			125			
His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	Ser
	130					135				140			
Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu	Leu
	145				150					155			160
Asp	Leu	Lys	Tyr	Val	Ala	Asp	Gly	Asp	Leu	Xaa	Leu	Arg	Thr
				165				170					175
His	Pro	Glu	Ser	Thr									
				180									

&lt;210&gt; 79

&lt;211&gt; 549

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Met IL-29 Asp19 Asp170 Cys172 mutant

&lt;221&gt; CDS

&lt;222&gt; (1)...(549)

&lt;221&gt; variation

&lt;222&gt; (515)...(516)

&lt;223&gt; n = A, T, G, or C

&lt;400&gt; 79

atg	ggc	cct	gtc	ccc	act	tcc	aag	ccc	acc	aca	act	ggg	aag	ggc	tgc	48
Met	Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	Lys	Gly	Cys	
1				5					10					15		

cac	att	gay	agg	ttc	aaa	tct	ctg	tca	cca	cag	gag	cta	gcg	agc	ttc	96
His	Ile	Asp	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	Ser	Phe	
			20					25					30			

aag	aag	gcc	agg	gac	gcc	ttg	gaa	gag	tca	ctc	aag	ctg	aaa	aac	tgg	144
Lys	Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	Asn	Trp	
		35				40						45				

agt	tgc	agc	tct	cct	gtc	ttc	ccc	ggg	aat	tgg	gac	ctg	agg	ctt	ctc	192
Ser	Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu	
	50					55					60					

cag	gtg	agg	gag	cgc	cct	gtg	gcc	ttg	gag	gct	gag	ctg	gcc	ctg	acg	240
Gln	Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Leu	Thr	
	65				70				75						80	

ctg	aag	gtc	ctg	gag	gcc	gct	gct	ggc	cca	gcc	ctg	gag	gac	gtc	cta	288
Leu	Lys	Val	Leu	Glu	Ala	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp	Val	Leu	
			85					90						95		

gac	cag	ccc	ctt	cac	acc	ctg	cac	cac	atc	ctc	tcc	cag	ctc	cag	gcc	336
Asp	Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu	Gln	Ala	
			100					105					110			

tgt	atc	cag	cct	cag	ccc	aca	gca	ggg	ccc	agg	ccc	cgg	ggc	cgc	ctc	384
Cys	Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly	Arg	Leu	
		115					120					125				

cac	cac	tgg	ctg	cac	cgg	ctc	cag	gag	gcc	ccc	aaa	aag	gag	tcc	gct	432
His	His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	Ser	Ala	
		130				135					140					

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 cga gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca 528  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser  
 165 170 175  
 acc cac cct gag tcc acc tga 549  
 Thr His Pro Glu Ser Thr \*  
 180

<210> 80  
 <211> 182  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Met IL-29 Asp19 Asp170 Cys172 mutant

<221> VARIANT  
 <222> (172)...(172)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 80  
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys  
 1 5 10 15  
 His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser  
 165 170 175  
 Thr His Pro Glu Ser Thr  
 180

<210> 81  
 <211> 546  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IL-29 Cys15 mutant Asp18 Asp169

<221> CDS  
 <222> (1)...(546)

<221> variation  
 <222> (44)...(45)

<223> n = A, T, G, or C

<400> 81  
 ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn cac 48  
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His  
 1 5 10 15  
 att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96  
 Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys  
 20 25 30  
 aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144  
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser  
 35 40 45  
 tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192  
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln  
 50 55 60  
 gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240  
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu  
 65 70 75 80  
 aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac 288  
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp  
 85 90 95  
 cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336  
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys  
 100 105 110  
 atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384  
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His  
 115 120 125  
 cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct gcc 432  
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly  
 130 135 140  
 tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480  
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
 145 150 155 160  
 gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca acc 528  
 Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr  
 165 170 175  
 cac cct gag tcc acc tga 546  
 His Pro Glu Ser Thr \*

<210> 82  
 <211> 181  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-29 Cys15 mutant Asp18 Asp169  
 <221> VARIANT  
 <222> (15)...(15)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 82



Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His  
 1 5 10 15  
 Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys  
 20 25 30  
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser  
 35 40 45  
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln  
 50 55 60  
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu  
 65 70 75 80  
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp  
 85 90 95  
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys  
 100 105 110  
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His  
 115 120 125  
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly  
 130 135 140  
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
 145 150 155 160  
 Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr  
 165 170 175  
 His Pro Glu Ser Thr  
 180

<210> 83  
 <211> 549  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Met IL-29 Cys16 mutant Asp19 Asp170

<221> CDS  
 <222> (1)...(549)

<221> variation  
 <222> (47)...(48)  
 <223> n = A, T, G, or C

<400> 83  
 atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn 48  
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa  
 1 5 10 15  
 cac att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96  
 His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144  
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca 528  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser  
 165 170 175

acc cac cct gag tcc acc tga 549  
 Thr His Pro Glu Ser Thr \*

<210> 84  
 <211> 182  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Met IL-29 Cys16 mutant Asp19 Asp170

<221> VARIANT  
 <222> (16)...(16)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 84  
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa  
 1 5 10 15  
 His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser  
 165 170 175  
 Thr His Pro Glu Ser Thr  
 180

<210> 85  
 <211> 528  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IL-28B Cys48 mutant

<221> CDS  
 <222> (1)...(528)

<221> variation  
 <222> (143)...(144)  
 <223> n = A, T, G, or C

<400> 85  
 gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc tgc 48  
 Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys 15  
 1 5 10  
 cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96  
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe 30  
 20 25  
 aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac dnn 144  
 Lys Arg Ala Lys Asp Ala Leu Glu Ser Leu Leu Leu Lys Asp Xaa 45  
 35 40  
 aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192  
 Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu 60  
 50 55  
 cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg acg 240  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr 80  
 65 70 75  
 ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg gat 288  
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly Asp 95  
 85 90  
 gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ctc 336  
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu 110  
 100 105  
 cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc 384  
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly 125  
 115 120  
 cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag gag 432  
 Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu 140  
 130 135  
 tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc 480  
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu 160  
 145 150 155  
 ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc tga 528  
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val \* 175  
 165 170

<210> 86  
 <211> 175  
 <212> PRT

<213> Artificial Sequence

<220>

<223> IL-28B Cys48 mutant

<221> VARIANT

<222> (48)...(48)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 86

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Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
1      5      10      15
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
20
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Xaa
35      40      45
Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
50      55      60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65      70      75      80
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly Asp
85      90      95
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
100      105      110
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
115      120      125
Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
130      135      140
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
145      150      155      160
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165      170      175

```

<210> 87

<211> 531

<212> DNA

<213> Artificial Sequence

<220>

<223> Met IL-28B Cys49 mutant

<221> CDS

<222> (1)...(531)

<221> variation

<222> (146)...(147)

<223> n = A, T, G, or C

<400> 87

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atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc 48
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
1      5      10      15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20      25      30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
35      40      45

dnn aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192
Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50      55      60

```

ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg 240  
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu  
 65 70 75 80

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg 288  
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly  
 85 90 95

gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336  
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln  
 100 105 110

ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg 384  
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg  
 115 120 125

ggc cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag 432  
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys  
 130 135 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480  
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg  
 145 150 155 160

ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc 528  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

tga 531  
 \*

<210> 88

<211> 176

<212> PRT

<213> Artificial Sequence

<220>

<223> Met IL-28B Cys49 mutant

<221> VARIANT

<222> (49)...(49)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 88

Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly  
 1 5 10 15  
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala  
 20 25 30  
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp  
 35 40 45  
 Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln  
 50 55 60  
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu  
 65 70 75 80  
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly  
 85 90 95  
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln  
 100 105 110  
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg  
 115 120 125  
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys  
 130 135 140

Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg  
 145 150 155 160  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

<210> 89  
 <211> 528  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IL-28B Cys50 mutant

<221> CDS  
 <222> (1)...(528)

<221> variation  
 <222> (149)...(150)  
 <223> n = A, T, G, or C

<400> 89  
 gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc tgc 48  
 Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys  
 1 5 10 15  
 cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96  
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe  
 20 25 30  
 aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tgc 144  
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Cys  
 35 40 45  
 aag dnn cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192  
 Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu  
 50 55 60  
 cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg acg 240  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg gat 288  
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly Asp  
 85 90 95  
 gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ctc 336  
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu  
 100 105 110  
 cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc 384  
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly  
 115 120 125  
 cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag gag 432  
 Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu  
 130 135 140  
 tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc 480  
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu  
 145 150 155 160  
 ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc tga 528  
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val \*  
 165 170 175

<210> 90  
 <211> 175  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-28B Cys50 mutant

<221> VARIANT  
 <222> (50)...(50)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 90  
 Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys  
 1 5 10 15  
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe  
 20 25 30  
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Cys  
 35 40 45  
 Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly Asp  
 85 90 95  
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu  
 100 105 110  
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly  
 115 120 125  
 Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu  
 130 135 140  
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu  
 145 150 155 160  
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

<210> 91  
 <211> 531  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Met IL-28B Cys51 mutant

<221> CDS  
 <222> (1)...(531)

<221> variation  
 <222> (152)...(153)  
 <223> n = A, T, G, or C

<400> 91  
 atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc 48  
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly 15  
 1 5 10  
 tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96  
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala 30  
 20 25  
 ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144

Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp  
 35 40 45  
 tgc aag dnn cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192  
 Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln  
 50 55 60  
 ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg 240  
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu  
 65 70 75 80  
 acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg 288  
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly  
 85 90 95  
 gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336  
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln  
 100 105 110  
 ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg 384  
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg  
 115 120 125  
 ggc cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag 432  
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys  
 130 135 140  
 gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480  
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg  
 145 150 155 160  
 ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc 528  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175  
 tga 531  
 \*

<210> 92  
 <211> 176  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> Met IL-28B Cys51 mutant  
 <221> VARIANT  
 <222> (51)...(51)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 92  
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly  
 1 5 10 15  
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala  
 20 25 30  
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp  
 35 40 45  
 Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln  
 50 55 60  
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu  
 65 70 75 80  
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly  
 85 90 95



Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln  
 100 105 110  
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg  
 115 120 125  
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys  
 130 135 140  
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg  
 145 150 155 160  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

<210> 93  
 <211> 528  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IL-28B Cys48 mutant T87S H135Y

<221> CDS  
 <222> (1)...(528)

<221> variation  
 <222> 143, 144, 261  
 <223> n = A, T, G, or C

<400> 93  
 gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc tgc 48  
 Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys  
 1 5 10 15  
 cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96  
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe  
 20 25 30  
 aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac dnn 144  
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Xaa  
 35 40 45  
 aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192  
 Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu  
 50 55 60  
 cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg acg 240  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 ctg aag gtt ctg gag gcc wsn gct gac act gac cca gcc ctg ggg gat 288  
 Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly Asp  
 85 90 95  
 gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ctc 336  
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu  
 100 105 110  
 cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc 384  
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly  
 115 120 125  
 cgc ctc cac cat tgg ctg tay cgg ctc cag gag gcc cca aaa aag gag 432  
 Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu  
 130 135 140  
 tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc 480

Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu  
 145 150 155 160  
 ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc tga 528  
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val \*  
 165 170 175

<210> 94  
 <211> 175  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> VARIANT  
 <222> (48)...(48)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<221> VARIANT  
 <222> (87)...(87)  
 <223> Xaa = Ser  
 <223> IL-28B Cys48 mutant T87S H135Y

<400> 94  
 Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys  
 1 5 10 15  
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe  
 20 25 30  
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Xaa  
 35 40 45  
 Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly Asp  
 85 90 95  
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu  
 100 105 110  
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly  
 115 120 125  
 Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu  
 130 135 140  
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu  
 145 150 155 160  
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

<210> 95  
 <211> 531  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Met IL-28B Cys49 mutant T88S H136Y

<221> CDS  
 <222> (1)...(531)  
 <221> variation  
 <222> 146, 147, 264  
 <223> n = A, T, G, or C

<400> 95  
 atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc 48  
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly  
 1 5 10 15  
 tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96  
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala  
 20 25 30  
 ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144  
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp  
 35 40 45  
 dnn aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192  
 Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln  
 50 55 60  
 ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg 240  
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu  
 65 70 75 80  
 acg ctg aag gtt ctg gag gcc wsn gct gac act gac cca gcc ctg ggg 288  
 Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly  
 85 90 95  
 gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336  
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln  
 100 105 110  
 ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg 384  
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg  
 115 120 125  
 ggc cgc ctc cac cat tgg ctg tay cgg ctc cag gag gcc cca aaa aag 432  
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys  
 130 135 140  
 gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480  
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg  
 145 150 155 160  
 ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc 528  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175  
 tga 531  
 \*

<210> 96  
 <211> 176  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> VARIANT  
 <222> (49)...(49)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<221> VARIANT  
 <222> (136)...(136)  
 <223> Xaa = Ser

<223> Met IL-28B Cys49 mutant T88S H136Y

&lt;400&gt; 96

```

Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
1      5      10      15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20      25      30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
35      40      45
Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50      55      60
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65      70      75      80
Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
85      90      95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100     105     110
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
115     120     125
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
130     135     140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145     150     155     160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165     170     175

```

&lt;210&gt; 97

&lt;211&gt; 528

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; IL-28B Cys50 mutant T87S H135Y

&lt;221&gt; CDS

&lt;222&gt; (1)...(528)

&lt;221&gt; variation

&lt;222&gt; 149, 150, 261

&lt;223&gt; n = A, T, G, or C

&lt;400&gt; 97

```

gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc tgc 48
Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
1      5      10      15
cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
20      25      30
aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tgc 144
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Cys
35      40      45
aag dnn cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192
Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
50      55      60
cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg acg 240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65      70      75      80
ctg aag gtt ctg gag gcc wsn gct gac act gac cca gcc ctg ggg gat 288
Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly Asp
85      90      95

```

gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ctc 336  
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu  
 100 105 110

cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc 384  
 Arg Ala Cys Ile Gln Pro Gln Thr Ala Gly Pro Arg Thr Arg Gly  
 115 120 125

cgc ctc cac cat tgg ctg tay cgg ctc cag gag gcc cca aaa aag gag 432  
 Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu  
 130 135 140

tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc 480  
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu  
 145 150 155 160

ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc tga 528  
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val \*  
 165 170 175

<210> 98

<211> 175

<212> PRT

<213> Artificial Sequence

<220>

<221> VARIANT

<222> (50)...(50)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<221> VARIANT

<222> (87)...(87)

<223> Xaa = Ser

<223> IL-28B Cys50 mutant T87S H135Y

<400> 98

Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys  
 1 5 10 15  
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe  
 20 25 30  
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Cys  
 35 40 45  
 Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly Asp  
 85 90 95  
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu  
 100 105 110  
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly  
 115 120 125  
 Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu  
 130 135 140  
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu  
 145 150 155 160  
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

<210> 99

<211> 531  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Met IL-28B Cys51 mutant T88S H136Y

<221> CDS  
 <222> (1)...(531)

<221> variation  
 <222> 152, 152, 264  
 <223> n = A, T, G, or C

```

<400> 99
atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc 48
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
1 5 10 15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20 25 30

ttt aag agg gcc aaa gat gcc tta gaa gag tgc ctt ctg ctg aag gac 144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
35 40 45

tgc aag dnn cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192
Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50 55 60

ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg 240
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65 70 75 80

acg ctg aag gtt ctg gag gcc wsn gct gac act gac cca gcc ctg ggg 288
Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
85 90 95

gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100 105 110

ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg 384
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
115 120 125

ggc cgc ctc cac cat tgg ctg tay cgg ctc cag gag gcc cca aaa aag 432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
130 135 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145 150 155 160

ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc 528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165 170 175

tga
*
```

531

<210> 100

<211> 176  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> VARIANT  
 <222> (51)...(51)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<221> VARIANT  
 <222> (88)...(88)  
 <223> Xaa = Ser

<223> Met IL-28B Cys51 mutant T88S H136Y

<400> 100  
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly  
 1 5 10 15  
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala  
 20 25 30  
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp  
 35 40 45  
 Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln  
 50 55 60  
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu  
 65 70 75 80  
 Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly  
 85 90 95  
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln  
 100 105 110  
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg  
 115 120 125  
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys  
 130 135 140  
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg  
 145 150 155 160  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

<210> 101  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> signal sequence

<221> CDS  
 <222> (1)...(45)

<221> variation  
 <222> 6, 9, 12, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45  
 <223> n = A, T, G, or C

<400> 101  
 atg gcn gcn gcn tgg acn gtn gtn ytn gtn acn ytn gtn ytn ggn 45  
 Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly  
 1 5 10 15

<210> 102  
 <211> 15  
 <212> PRT

<213> Artificial Sequence

<220>

<223> signal sequence

<400> 102

Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly  
1 5 10 15

<210> 103

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> signal sequence

<221> CDS

<222> (1)...(57)

<221> variation

<222> 6, 9, 12, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 48, 51,  
54, 57

<223> n = A, T, G, or C

<400> 103

atg gcn gcn gcn tgg acn gtn gtn ytn gtn acn ytn gtn ytn ggn ytn 48  
Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu  
1 5 10 15

gcn gtn gcn  
Ala Val Ala

<210> 104

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> signal sequence

<400> 104

Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu  
1 5 10 15  
Ala Val Ala

<210> 105

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> signal sequence

<221> CDS

<222> (1)...(63)

<221> variation

<222> 6, 9, 12, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 48, 51,  
54, 57, 60, 63



<223> n = A, T, G, or C

<400> 105  
 atg gcn gcn gcn tgg acn gtn gtn ytn gtn acn ytn gtn ytn ggn ytn 48  
 Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu  
 1 5 10 15  
 gcn gtn gcn ggn ccn 63  
 Ala Val Ala Gly Pro  
 20

<210> 106  
 <211> 21  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> signal sequence

<400> 106  
 Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu  
 1 5 10 15  
 Ala Val Ala Gly Pro  
 20

<210> 107  
 <211> 72  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> signal sequence

<221> CDS  
 <222> (1)...(72)

<221> variation  
 <222> 6, 9, 12, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 48, 51,  
 54, 57, 60, 63, 66, 69, 72  
 <223> n = A, T, G, or C

<400> 107  
 atg gcn gcn gcn tgg acn gtn gtn ytn gtn acn ytn gtn ytn ggn ytn 48  
 Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu  
 1 5 10 15  
 gcn gtn gcn ggn ccn gtn ccn acn 72  
 Ala Val Ala Gly Pro Val Pro Thr  
 20

<210> 108  
 <211> 24  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> signal sequence

<400> 108  
 Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu  
 1 5 10 15  
 Ala Val Ala Gly Pro Val Pro Thr

20

<210> 109  
 <211> 546  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IL-29 C171X

<221> CDS  
 <222> (1)...(546)

<221> variation  
 <222> (512)...(513)  
 <223> n = A, T, G, or C

<400> 109  
 ggt ccg gtt ccg acc tct aaa cca acc acc act ggt aaa ggt tgc cac 48  
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His  
 1 5 10 15  
 atc ggt cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc aaa 96  
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys  
 20 25 30  
 aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg tct 144  
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser  
 35 40 45  
 tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg cag 192  
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln  
 50 55 60  
 gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc ctg 240  
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu  
 65 70 75 80  
 aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg gat 288  
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp  
 85 90 95  
 cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct tgc 336  
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys  
 100 105 110  
 att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg cac 384  
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His  
 115 120 125  
 cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct ggt 432  
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly  
 130 135 140  
 tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc cgt 480  
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
 145 150 155 160  
 gat ctg aaa tac gtt gct gat ggt aac ctg dnn ctg cgt acc tct acc 528  
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr  
 165 170 175  
 cat ccg gaa tct acc taa 546  
 His Pro Glu Ser Thr \*

180

<210> 110  
 <211> 181  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-29 C171X

<221> VARIANT  
 <222> (171)...(171)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 110  
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His  
 1 5 10 15  
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys  
 20 25 30  
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser  
 35 40 45  
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln  
 50 55 60  
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu  
 65 70 75 80  
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp  
 85 90 95  
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys  
 100 105 110  
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His  
 115 120 125  
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly  
 130 135 140  
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg  
 145 150 155 160  
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr  
 165 170 175  
 His Pro Glu Ser Thr  
 180

<210> 111  
 <211> 549  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Met IL-29 C172X

<221> CDS  
 <222> (1)...(549)

<221> variation  
 <222> (515)...(516)  
 <223> n = A, T, G, or C

<400> 111  
 atg ggt ccg gtt ccg acc tct aaa cca acc acc act ggt aaa ggt tgc 48  
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys  
 1 5 10 15  
 cac atc ggt cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc 96  
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30

aaa aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg 144  
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
35 40 45

tct tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg 192  
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
50 55 60

cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc 240  
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
65 70 75 80

ctg aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg 288  
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
85 90 95

gat cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct 336  
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
100 105 110

tgc att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg 384  
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
115 120 125

cac cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct 432  
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
130 135 140

ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc 48  
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
145 150 155 160

cgt gat ctg aaa tac gtt gct gat ggt aac ctg dnn ctg cgt acc tct 52  
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser  
165 170 175

acc cat ccg gaa tct acc taa  
Thr His Pro Glu Ser Thr \*

```
<210> 112
<211> 182
<212> PRT
<213> Artificial Sequence
```

<220>  
<223> Met IL-29 C172X

```
<221> VARIANT
<222> (172)...(172)
<223> Xaa = Ser, Ala, Thr, Val, or Asn
```

<400> 112															
Met	Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	Lys	Gly	Cys
1				5					10					15	
His	Ile	Gly	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	Ser	Phe
			20					25					30		
Lys	Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	Asn	Trp
		35				40						45			
Ser	Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu
	50					55					60				
Gln	Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Leu	Thr
65					70					75					80

Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser  
 165 170 175  
 Thr His Pro Glu Ser Thr  
 180

<210> 113

<211> 543

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29 C170X, truncated after N-terminal Methionine  
and Glycine

<221> CDS

<222> (1)...(543)

<221> variation

<222> (509)...(510)

<223> n = A, T, G, or C

<400> 113

cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att 48  
 Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile  
 1 5 10 15  
 ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag 96  
 Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys  
 20 25 30  
 gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc 144  
 Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys  
 35 40 45  
 agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg 192  
 Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val  
 50 55 60  
 agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag 240  
 Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys  
 65 70 75 80  
 gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag 288  
 Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln  
 85 90 95  
 ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc 336  
 Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile  
 100 105 110  
 cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac 384  
 Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His  
 115 120 125

tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc 432  
 Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys  
 130 135 140

ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac 480  
 Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp  
 145 150 155 160

ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc cac 528  
 Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His  
 165 170 175

cct gag tcc acc tga 543  
 Pro Glu Ser Thr \*  
 180

<210> 114  
 <211> 180  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-29 C170X, truncated after N-terminal Methionine  
 and Glycine

<221> VARIANT  
 <222> (170)...(170)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 114  
 Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile  
 1 5 10 15  
 Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys  
 20 25 30  
 Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys  
 35 40 45  
 Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val  
 50 55 60  
 Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys  
 65 70 75 80  
 Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln  
 85 90 95  
 Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile  
 100 105 110  
 Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His  
 115 120 125  
 Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys  
 130 135 140  
 Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp  
 145 150 155 160  
 Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His  
 165 170 175  
 Pro Glu Ser Thr  
 180

<210> 115  
 <211> 540  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IL-29 C169X, truncated after N-terminal

## Methionine, Glycine, and Proline

&lt;221&gt; CDS

&lt;222&gt; (1)...(540)

&lt;221&gt; variation

&lt;222&gt; (506)...(507)

&lt;223&gt; n = A, T, G, or C

&lt;400&gt; 115

gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc 48  
 Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly 15

agg ttc aaa tct ctg tca cca cag gag cta ggc agc ttc aag aag gcc 96  
 Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala 30

agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc 144  
 Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser 45

tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg 192  
 Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg 60

gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc 240  
 Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val 80

ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc 288  
 Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro 95

ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag 336  
 Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln 110

cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg 384  
 Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp 125

ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg 432  
 Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu 140

gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc 480  
 Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu 160

aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct 528  
 Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro 175

gag tcc acc tga 540  
 Glu Ser Thr \*

&lt;210&gt; 116

&lt;211&gt; 179

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> IL-29 C169X, truncated after N-terminal  
Methionine, Glycine, and Proline

<221> VARIANT

<222> (169)....(169)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 116  
Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly  
1 5 10 15  
Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala  
20 25 30  
Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser  
35 40 45  
Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg  
50 55 60  
Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val  
65 70 75 80  
Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro  
85 90 95  
Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln  
100 105 110  
Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp  
115 120 125  
Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu  
130 135 140  
Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu  
145 150 155 160  
Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro  
165 170 175  
Glu Ser Thr

<210> 117

<211> 537

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29 C168X, truncated after N-terminal  
Methionine, Glycine, Proline, and Valine

<221> CDS

<222> (1)...(537)

<221> variation

<222> (503)...(504)

<223> n = A, T, G, or C

<400> 117  
ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg 48  
Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg  
1 5 10 15  
ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg 96  
Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg  
20 25 30  
gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct 144  
Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser  
35 40 45  
cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag 192  
Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu



50

55

60

cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg 240  
 Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu 80  
 65 70 75

gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt 288  
 Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu 95  
 85 90

cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct 336  
 His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro 110  
 100 105

cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg 384  
 Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu 125  
 115 120

cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag 432  
 His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu 140  
 130 135

gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa 480  
 Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys 160  
 145 150 155

tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag 528  
 Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu 175  
 165 170

tcc acc tga 537  
 Ser Thr \*

<210> 118  
 <211> 178  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-29 C168X, truncated after N-terminal  
 Methionine, Glycine, Proline, and Valine

<221> VARIANT  
 <222> (168)...(168)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 118  
 Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg 15  
 1 5 10  
 Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg 30  
 20 25  
 Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser 45  
 35 40  
 Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu 60  
 50 55 60  
 Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu 80  
 65 70 75  
 Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu 95  
 85 90  
 His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro 110  
 100 105  
 Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu 125  
 115 120

His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu  
 130 135 140  
 Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys  
 145 150 155 160  
 Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu  
 165 170 175  
 Ser Thr

<210> 119

<211> 534

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29 C167X, truncated after N-terminal  
 Methionine, Glycine, Proline, Valine, and Proline

<221> CDS

<222> (1)... (534)

<221> variation

<222> (500)... (501)

<223> n = A, T, G, or C

<400> 119

act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg ttc 48  
 Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe  
 1 5 10 15

aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg gac 96  
 Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp  
 20 25 30

gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct cct 144  
 Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro  
 35 40 45

gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag cgc 192  
 Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg  
 50 55 60

cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg gag 240  
 Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu  
 65 70 75 80

gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt cac 288  
 Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His  
 85 90 95

acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct cag 336  
 Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln  
 100 105 110

ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg cac 384  
 Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His  
 115 120 125

cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag gca 432  
 Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala  
 130 135 140

tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa tat 480  
 Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr



&lt;222&gt; (497)...(498)

&lt;223&gt; n = A, T, G, or C

&lt;400&gt; 121

tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg ttc aaa 48  
 Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys 15  
 1 5 10

tct ctg tca cca cag gag cta ggc agc ttc aag aag gcc agg gac gcc 96  
 Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala 30  
 20 25

ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct cct gtc 144  
 Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val 45  
 35 40

ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag cgc cct 192  
 Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro 60  
 50 55

gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg gag gcc 240  
 Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala 80  
 65 70 75

gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt cac acc 288  
 Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr 95  
 85 90

ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct cag ccc 336  
 Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro 110  
 100 105

aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg cac cgg 384  
 Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg 125  
 115 120

ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag gca tct 432  
 Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser 140  
 130 135

gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa tat gtg 480  
 Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val 160  
 145 150 155

gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag tcc acc 528  
 Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr 175  
 165 170

531

tga

\*

&lt;210&gt; 122

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> IL-29 C166X, truncated after N-terminal  
 Methionine, Glycine, Proline, Valine, Proline, and  
 Threonine

&lt;221&gt; VARIANT

&lt;222&gt; (166)...(166)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 122  
 Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys  
 1 5 10 15  
 Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala  
 20 25 30  
 Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val  
 35 40 45  
 Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro  
 50 55 60  
 Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala  
 65 70 75 80  
 Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr  
 85 90 95  
 Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro  
 100 105 110  
 Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg  
 115 120 125  
 Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser  
 130 135 140  
 Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val  
 145 150 155 160  
 Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr  
 165 170 175

<210> 123

<211> 528

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29 C165X, truncated after N-terminal  
 Methionine, Glycine, Proline, Valine, Proline,  
 Threonine, and Serine

<221> CDS

<222> (1)...(528)

<221> variation

<222> (494)...(495)

<223> n = A, T, G, or C

<400> 123

aag ccc acc aca act ggg aag ggc tgc cac att ggc agg ttc aaa tct 48  
 Lys Pro Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys Ser  
 1 5 10 15

ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg gac gcc ttg 96  
 Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu  
 20 25 30

gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct cct gtc ttc 144  
 Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val Phe  
 35 40 45

ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag cgc cct gtg 192  
 Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro Val  
 50 55 60

gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg gag gcc gct 240  
 Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Ala  
 65 70 75 80

gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt cac acc ctg 288  
 Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr Leu 95  
 85

cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct cag ccc aca 336  
 His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro Thr 110  
 100 105

gca ggg ccc agg ccc cgg gcc cgc ctc cac cac tgg ctg cac cgg ctc 384  
 Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg Leu 125  
 115 120

cag gag gcc ccc aaa aag gag tcc gct gcc tgc ctg gag gca tct gtc 432  
 Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser Val 140  
 130 135

acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa tat gtg gcc 480  
 Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val Ala 160  
 145 150 155

gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag tcc acc tga 528  
 Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr \* 175  
 165 170

<210> 124

<211> 175

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 C165X, truncated after N-terminal  
 Methionine, Glycine, Proline, Valine, Proline,  
 Threonine, and Serine

<221> VARIANT

<222> (165)...(165)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 124

Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys Ser 15  
 1 5 10  
 Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu 30  
 20 25  
 Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val Phe 45  
 35 40  
 Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro Val 60  
 50 55 60  
 Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Ala 80  
 65 70 75  
 Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr Leu 95  
 85 90  
 His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro Thr 110  
 100 105  
 Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg Leu 125  
 115 120  
 Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser Val 140  
 130 135  
 Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val Ala 160  
 145 150 155  
 Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr 175  
 165 170

<210> 125  
 <211> 552  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IL-29 Leu insert after N-terminal Met, C173X

<221> CDS  
 <222> (1)...(552)

<221> variation  
 <222> (6)...(6)  
 <223> n = A, T, G, or C

<221> variation  
 <222> (518)...(519)  
 <223> n = A, T, G, or C

<400> 125  
 atg ytn ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc 48  
 Met Leu Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly 15  
 1 5 10  
 tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc 96  
 Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser 30  
 20 25  
 ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac 144  
 Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn 45  
 35 40  
 tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt 192  
 Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu 60  
 50 55  
 ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg 240  
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu 75 80  
 65 70  
 acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc 288  
 Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val 90 95  
 85  
 cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag 336  
 Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln 110  
 100 105  
 gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc 384  
 Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg 125  
 115 120  
 ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc 432  
 Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser 140  
 130 135  
 gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc 480  
 Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu 155 160  
 145 150  
 acg cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg 528  
 Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr 170 175  
 165  
 tca acc cac cct gag tcc acc tga 552

Ser Thr His Pro Glu Ser Thr \*  
180

<210> 126  
<211> 183  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> IL-29 Leu insert after N-terminal Met, C173X

<221> VARIANT  
<222> (173)...(173)  
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 126  
Met Leu Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly  
1 10 15  
Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser  
20 25 30  
Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn  
35 40 45  
Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu  
50 55 60  
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu  
65 70 75 80  
Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val  
85 90 95  
Leu Asp Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Leu Gln  
100 105 110  
Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg  
115 120 125  
Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser  
130 135 140  
Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu  
145 150 155 160  
Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr  
165 170 175  
Ser Thr His Pro Glu Ser Thr  
180

<210> 127  
<211> 549  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> IL-29 G2L C172X

<221> CDS  
<222> (1)...(549)

<221> variation  
<222> (6)...(6)  
<223> n = A, T, G, or C

<221> variation  
<222> (515)...(516)  
<223> n = A, T, G, or C

<400> 127  
atg ytn cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc 48.  
Met Leu Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys



1	5	10	15	
cac att ggc agg ttc aaa tct ctg tca cca cag gag cta ggc agc ttc	96			
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe				
20 25 30				
aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg	144			
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp				
35 40 45				
agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc	192			
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu				
50 55 60				
cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg	240			
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr				
65 70 75 80				
ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta	288			
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu				
85 90 95				
gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc	336			
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala				
100 105 110				
tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg gcc cgc ctc	384			
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu				
115 120 125				
cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct	432			
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala				
130 135 140				
ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg	480			
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr				
145 150 155 160				
cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca	528			
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser				
165 170 175				
acc cac cct gag tcc acc tga	549			
Thr His Pro Glu Ser Thr *				
180				

<210> 128  
 <211> 182  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-29 G2L C172X

<221> VARIANT  
 <222> (172)...(172)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 128  
 Met Leu Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys  
 1 5 10 15  
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp

35 40 45  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser  
 165 170 175  
 Thr His Pro Glu Ser Thr  
 180

<210> 129  
 <211> 552  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IL-29 Ile insert after N-terminal Met, C173X

<221> CDS  
 <222> (1)...(552)

<221> variation  
 <222> (518)...(519)  
 <223> n = A, T, G, or C

<400> 129  
 atg ath ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc 48  
 Met Ile Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly  
 1 5 10 15  
 tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc 96  
 Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser  
 20 25 30  
 ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac 144  
 Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn  
 35 40 45  
 tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt 192  
 Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu  
 50 55 60  
 ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg 240  
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu  
 65 70 75 80  
 acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc 288  
 Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val  
 85 90 95  
 cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag 336  
 Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln  
 100 105 110

gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc 384  
 Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg  
 115 120 125

ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc 432  
 Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser  
 130 135 140

gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc 480  
 Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu  
 145 150 155 160

acg cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg 528  
 Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr  
 165 170 175

tca acc cac cct gag tcc acc tga 552  
 Ser Thr His Pro Glu Ser Thr \*  
 180

<210> 130  
 <211> 183  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-29 Ile insert after N-terminal Met, C173X

<221> VARIANT  
 <222> (173)...(173)  
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 130  
 Met Ile Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly  
 1 5 10 15  
 Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser  
 20 25 30  
 Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn  
 35 40 45  
 Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu  
 50 55 60  
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu  
 65 70 75 80  
 Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val  
 85 90 95  
 Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln  
 100 105 110  
 Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg  
 115 120 125  
 Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser  
 130 135 140  
 Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu  
 145 150 155 160  
 Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr  
 165 170 175  
 Ser Thr His Pro Glu Ser Thr  
 180

<210> 131  
 <211> 549  
 <212> DNA  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; IL-29 G2I C172X

&lt;221&gt; CDS

&lt;222&gt; (1)...(549)

&lt;221&gt; variation

&lt;222&gt; (515)...(516)

&lt;223&gt; n = A, T, G, or C

&lt;400&gt; 131

```

atg ath cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc 48
Met Ile Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
1 5 10 15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
115 120 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca 528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
165 170 175

acc cac cct gag tcc acc tga 549
Thr His Pro Glu Ser Thr *
180

```

&lt;210&gt; 132

&lt;211&gt; 182

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; IL-29 G2I C172X

&lt;221&gt; VARIANT

&lt;222&gt; (172)...(172)

&lt;223&gt; Xaa = Ser, Ala, Thr, Val, or Asn

&lt;400&gt; 132

```

Met Ile Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
1          5          10          15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20          25          30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35          40          45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50          55          60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65          70          75
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85          90          95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
100          105          110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
115          120          125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
130          135          140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145          150          155
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
165          170          175
Thr His Pro Glu Ser Thr
180

```

&lt;210&gt; 133

&lt;211&gt; 531

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> IL-29 after N-terminal Met amino acid residues 2-7  
deleted, C166X

&lt;221&gt; CDS

&lt;222&gt; (1)...(531)

&lt;221&gt; variation

&lt;222&gt; (497)...(498)

&lt;223&gt; n = A, T, G, or C

&lt;400&gt; 133

```

atg aag ccc acc aca act ggg aag ggc tgc cac att ggc agg ttc aaa 48
Met Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys
1          5          10          15
tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg gac gcc 96
Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala
20          25          30
ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct cct gtc 144
Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val
35          40          45
ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag cgc cct 192
Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro

```

50

55

60

gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg gag gcc 240  
 Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala  
 65 70 75 80

gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt cac acc 288  
 Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr  
 85 90 95

ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct cag ccc 336  
 Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro  
 100 105 110

aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg cac cgg 384  
 Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg  
 115 120 125

ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag gca tct 432  
 Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser  
 130 135 140

gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa tat gtg 480  
 Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val  
 145 150 155 160

gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag tcc acc 528  
 Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr  
 165 170 175

tga 531  
 \*

&lt;210&gt; 134

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> IL-29 after N-terminal Met amino acid residues 2-7 -  
 deleted, C166X

&lt;221&gt; VARIANT

&lt;222&gt; (166)...(166)

&lt;223&gt; Xaa = Ser, Ala, Thr, Val, or Asn

&lt;400&gt; 134

Met Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys  
 1 5 10 15  
 Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala  
 20 25 30  
 Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Pro Val  
 35 40 45  
 Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro  
 50 55 60  
 Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala  
 65 70 75 80  
 Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr  
 85 90 95  
 Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro  
 100 105 110  
 Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg  
 115 120 125

Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser  
 130 135 140  
 Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val  
 145 150 155 160  
 Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr  
 165 170 175

<210> 135

<211> 558

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29 Glu, Ala, and Glu inserted after N-terminal  
 Met, C175X

<221> CDS

<222> (1) ... (558)

<221> variation

<222> (524) ... (525)

<223> n = A, T, G, or C

<400> 135

atg gar gcn gar ggc cct gtc ccc act tcc aag ccc acc aca act ggg 48  
 Met Glu Ala Glu Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly  
 1 5 10 15

aag ggc tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta 96  
 Lys Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu  
 20 25 30

gcg agc ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg 144  
 Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu  
 35 40 45

aaa aac tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg 192  
 Lys Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu  
 50 55 60

agg ctt ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg 240  
 Arg Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu  
 65 70 75 80

gcc ctg acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag 288  
 Ala Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu  
 85 90 95

gac gtc cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag 336  
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln  
 100 105 110

ctc cag gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg 384  
 Leu Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg  
 115 120 125

ggc cgc ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag 432  
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys  
 130 135 140

gag tcc gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc 480  
 Glu Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg  
 145 150 155 160

ctc ctc acg cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg 528  
 Leu Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu 175  
 165 170

aga acg tca acc cac cct gag tcc acc tga 558  
 Arg Thr Ser Thr His Pro Glu Ser Thr \*  
 180 185

<210> 136

<211> 185

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 Glu, Ala, and Glu inserted after N-terminal  
 Met, C175X

<221> VARIANT

<222> (175)...(175)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 136

Met	Glu	Ala	Glu	Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	
1				5					10						15	
Lys	Gly	Cys	His	Ile	Gly	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	
			20					25					30			
Ala	Ser	Phe	Lys	Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	
		35					40					45				
Lys	Asn	Trp	Ser	Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	
	50					55					60					
Arg	Leu	Leu	Gln	Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	
	65				70				75					80		
Ala	Leu	Thr	Leu	Lys	Val	Leu	Glu	Ala	Ala	Ala	Gly	Pro	Ala	Leu	Glu	
			85					90					95			
Asp	Val	Leu	Asp	Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	
			100					105					110			
Leu	Gln	Ala	Cys	Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	
		115					120					125				
Gly	Arg	Leu	His	His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	
	130					135					140					
Glu	Ser	Ala	Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	
	145				150				155					160		
Leu	Leu	Thr	Arg	Asp	Leu	Lys	Tyr	Val	Ala	Asp	Gly	Asn	Leu	Xaa	Leu	
			165					170						175		
Arg	Thr	Ser	Thr	His	Pro	Glu	Ser	Thr								
			180					185								

<210> 137

<211> 528

<212> DNA

<213> Artificial Sequence

<220>

<223> Human IL-28A C2 mutant for expression in E. coli

<221> CDS

<222> (1)...(528)

<221> variation

<222> (146)...(147)

<223> n = A, T, G or C

<400> 137



atg gtt ccg gtt gct cgt ctg cac ggt gct ctg ccg gac gct cgt ggt 48  
 Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly 15  
 1 5 10

tgc cac atc gct cag ttc aaa tct ctg tct ccg cag gaa ctg cag gct 96  
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala 30  
 20 25

ttc aaa cgt gct aaa gac gct ctg gaa gaa tct ctg ctg ctg aaa gac 144  
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp 45  
 35 40

dnn cgt tgc cac tct cgt ctg ttc ccg cgt acc tgg gac ctg cgt cag 192  
 Xaa Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln 60  
 50 55

ctg cag gtt cgt gaa cgt ccg atg gct ctg gaa gct gaa ctg gct ctg 240  
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu 80  
 65 70 75

acc ctg aaa gtt ctg gaa gct acc gct gac acc gac ccg gct ctg gtt 288  
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val 95  
 85 90

gac gtt ctg gac cag ccg ctg cac acc ctg cac cac atc ctg tct cag 336  
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln 110  
 100 105

ttc cgt gct tgc atc cag ccg cag ccg acc gct ggt ccg cgt acc cgt 384  
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg 125  
 115 120

ggt cgt ctg cac cac tgg ctg tac cgt ctg cag gaa gct ccg aaa aaa 432  
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys 140  
 130 135

gaa tct ccg ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt 480  
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg 160  
 145 150 155

ctg ctg acc cgt gac ctg aac tgc gtt gct tct ggt gac ctg tgc gtt 528  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val 175  
 165 170

<210> 138

<211> 176

<212> PRT

<213> Artificial Sequence

<220>

<223> Human IL-28A C2 mutant for expression in E. coli

<221> VARIANT

<222> (49)...(49)

<223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 138

Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly 15  
 1 5 10  
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala 30  
 20 25  
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp 45  
 35 40

Xaa Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln  
 50 55 60  
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu  
 65 70 75 80  
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val  
 85 90 95  
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln  
 100 105 110  
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg  
 115 120 125  
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys  
 130 135 140  
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg  
 145 150 155 160  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

<210> 139  
 <211> 528  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human IL-28A C3 mutant for expression in E. coli

<221> CDS  
 <222> (1)...(528)

<221> variation  
 <222> (152)...(153)  
 <223> n = A, T, G or C

<400> 139  
 atg gtt ccg gtt gct cgt ctg cac ggt gct ctg ccg gac gct cgt ggt 48  
 Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly  
 1 5 10 15  
 tgc cac atc gct cag ttc aaa tct ctg tct ccg cag gaa ctg cag gct 96  
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala  
 20 25 30  
 ttc aaa cgt gct aaa gac gct ctg gaa gaa tct ctg ctg ctg aaa gac 144  
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp  
 35 40 45  
 tgc cgt dnn cac tct cgt ctg ttc ccg cgt acc tgg gac ctg cgt cag 192  
 Cys Arg Xaa His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln  
 50 55 60  
 ctg cag gtt cgt gaa cgt ccg atg gct ctg gaa gct gaa ctg gct ctg 240  
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu  
 65 70 75 80  
 acc ctg aaa gtt ctg gaa gct acc gct gac acc gac ccg gct ctg gtt 288  
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val  
 85 90 95  
 gac gtt ctg gac cag ccg ctg cac acc ctg cac cac atc ctg tct cag 336  
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln  
 100 105 110  
 ttc cgt gct tgc atc cag ccg cag ccg acc gct ggt ccg cgt acc cgt 384  
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg  
 115 120 125

ggt cgt ctg cac cac tgg ctg tac cgt ctg cag gaa gct ccg aaa aaa 432  
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys  
 130 135 140  
 gaa tct ccg ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt 480  
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg  
 145 150 155 160  
 ctg ctg acc cgt gac ctg aac tgc gtt gct tct ggt gac ctg tgc gtt 528  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

<210> 140  
 <211> 176  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Human IL-28A C3 mutant for expression in E. coli  
 <221> VARIANT  
 <222> (51)...(51)  
 <223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 140  
 Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly  
 1 5 10 15  
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala  
 20 25 30  
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp  
 35 40 45  
 Cys Arg Xaa His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln  
 50 55 60  
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu  
 65 70 75 80  
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val  
 85 90 95  
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln  
 100 105 110  
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg  
 115 120 125  
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys  
 130 135 140  
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg  
 145 150 155 160  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

<210> 141  
 <211> 528  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human IL-28B C2 mutant for expression in E. coli  
 <221> CDS  
 <222> (1)...(528)  
 <221> variation  
 <222> 146, 147, 264

<223> n = A, T, G or C

<400> 141  
 atg gtt ccg gtt gct cgt ctg cgt ggt gct ctg ccg gac gct cgt ggt 48  
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly 15  
 1 5 10

tgc cac atc gct cag ttc aaa tct ctg tct ccg cag gaa ctg cag gct 96  
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala 30  
 20 25

ttc aaa cgt gct aaa gac gct ctg gaa gaa tct ctg ctg ctg aaa gac 144  
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp 45  
 35 40

dnn aaa tgc cgt tct cgt ctg ttc ccg cgt acc tgg gac ctg cgt cag 192  
 Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln 60  
 50 55

ctg cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg 240  
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu 80  
 65 70 75

acc ctg aaa gtt ctg gaa gct wsn gct gac acc gac ccg gct ctg ggt 288  
 Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly 95  
 85 90

gac gtt ctg gac cag ccg ctg cac acc ctg cac cac atc ctg tct cag 336  
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln 110  
 100 105

ctg cgt gct tgc atc cag ccg cag ccg acc gct ggt ccg cgt acc cgt 384  
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg 125  
 115 120

ggt cgt ctg cac cac tgg ctg yay cgt ctg cag gaa gct ccg aaa aaa 432  
 Gly Arg Leu His His Trp Leu Xaa Arg Leu Gln Glu Ala Pro Lys Lys 140  
 130 135

gaa tct ccg ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt 480  
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg 160  
 145 150 155

ctg ctg acc cgt gac ctg aac tgc gtt gct tct ggt gac ctg tgc gtt 528  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val 175  
 165 170

<210> 142

<211> 176

<212> PRT

<213> Artificial Sequence

<220>

<223> Human IL-28B C2 mutant for expression in E. coli

<221> VARIANT

<222> (49)...(49)

<223> Xaa = Ser, Ala, Thr, Val or Asn

<221> VARIANT

<222> (88)...(88)

<223> Xaa = Thr or Ser

<221> VARIANT  
 <222> (136)...(136)  
 <223> Xaa = His or Tyr

<400> 142  
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly  
 1 5 10 15  
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala  
 20 25 30  
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp  
 35 40 45  
 Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln  
 50 55 60  
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu  
 65 70 75 80  
 Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly  
 85 90 95  
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln  
 100 105 110  
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg  
 115 120 125  
 Gly Arg Leu His His Trp Leu Xaa Arg Leu Gln Glu Ala Pro Lys Lys  
 130 135 140  
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg  
 145 150 155 160  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

<210> 143  
 <211> 528  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human IL-28B C3 mutant for expression in E. coli

<221> CDS  
 <222> (1)...(528)

<221> variation  
 <222> 152, 153, 264  
 <223> n = A, T, G or C

<400> 143  
 atg gtt ccg gtt gct cgt ctg cgt ggt gct ctg ccg gac gct cgt ggt 48  
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly  
 1 5 10 15  
 tgc cac atc gct cag ttc aaa tct ctg tct ccg cag gaa ctg cag gct 96  
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala  
 20 25 30  
 ttc aaa cgt gct aaa gac gct ctg gaa gaa tct ctg ctg ctg aaa gac 144  
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp  
 35 40 45  
 tgc aaa dnn cgt tct cgt ctg ttc ccg cgt acc tgg gac ctg cgt cag 192  
 Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln  
 50 55 60  
 ctg cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg 240  
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu  
 65 70 75 80

acc ctg aaa gtt ctg gaa gct wsn gct gac acc gac ccg gct ctg ggt 288  
 Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly  
 85 90 95

gac gtt ctg gac cag ccg ctg cac acc ctg cac cac atc ctg tct cag 336  
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln  
 100 105 110

ctg cgt gct tgc atc cag ccg cag ccg acc gct ggt ccg cgt acc cgt 384  
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg  
 115 120 125

ggt cgt ctg cac cac tgg ctg yay cgt ctg cag gaa gct ccg aaa aaa 432  
 Gly Arg Leu His His Trp Leu Xaa Arg Leu Gln Glu Ala Pro Lys Lys  
 130 135 140

gaa tct ccg ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt 480  
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg  
 145 150 155 160

ctg ctg acc cgt gac ctg aac tgc gtt gct tct ggt gac ctg tgc gtt 528  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

<210> 144  
 <211> 176  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Human IL-28B C3 mutant for expression in E. coli

<221> VARIANT  
 <222> (51)...(51)  
 <223> Xaa = Ser, Ala, Thr, Val or Asn

<221> VARIANT  
 <222> (88)...(88)  
 <223> Xaa = Thr or Ser

<221> VARIANT  
 <222> (136)...(136)  
 <223> Xaa = His or Tyr

<400> 144  
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly  
 1 5 10 15  
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala  
 20 25 30  
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp  
 35 40 45  
 Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln  
 50 55 60  
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu  
 65 70 75 80  
 Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly  
 85 90 95  
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln  
 100 105 110  
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg  
 115 120 125  
 Gly Arg Leu His His Trp Leu Xaa Arg Leu Gln Glu Ala Pro Lys Lys  
 130 135 140

Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg  
 145 150 155 160  
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  
 165 170 175

<210> 145  
 <211> 549  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human IL-29 C1 mutant for expression in E. coli

<221> CDS  
 <222> (1) ... (549)

<221> variation  
 <222> 33, 47, 48, 57  
 <223> n = A, T, G or C

<400> 145  
 atg ggt ccg gtt ccg acc tct aaa cca acc mcn act ggt aaa ggt dnn 48  
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Xaa Thr Gly Lys Gly Xaa  
 1 5 10 15  
 cac atc ggn cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc 96  
 His Ile Xaa Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 aaa aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg 144  
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 tct tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg 192  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc 240  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 ctg aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg 288  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 gat cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct 336  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 tgc att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg 384  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 cac cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct 432  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc 480  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 cgt gat ctg aaa tac gtt gct gat ggt ray ctg tgc ctg cgt acc tct 528  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Xaa Leu Cys Leu Arg Thr Ser  
 165 170 175

acc cat ccg gaa tct acc taa  
 Thr His Pro Glu Ser Thr \*  
 180

<210> 146  
 <211> 182  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Human IL-29 C1 mutant for expression in E. coli

<221> VARIANT  
 <222> (11)...(11)  
 <223> Xaa = Thr or Pro

<221> VARIANT  
 <222> (16)...(16)  
 <223> Xaa = Ser, Ala, Thr, Val or Asn

<221> VARIANT  
 <222> (19)...(19)  
 <223> Xaa = Gly or Asp

<221> VARIANT  
 <222> (170)...(170)  
 <223> Xaa = Asn or Asp

<400> 146  
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Xaa Thr Gly Lys Gly Xaa  
 1 5 10 15  
 His Ile Xaa Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Xaa Leu Cys Leu Arg Thr Ser  
 165 170 175  
 Thr His Pro Glu Ser Thr  
 180

<210> 147  
 <211> 549  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human IL-29 C5 mutant for expression in E. coli



<221> CDS  
 <222> (1)...(549)

<221> variation  
 <222> 33, 57, 515, 516  
 <223> n = A, T, G or C

<400> 147  
 atg ggt ccg gtt ccg acc tct aaa cca acc mcn act ggt aaa ggt tgc 48  
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Xaa Thr Gly Lys Gly Cys  
 1 5 10 15

cac atc grn cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc 96  
 His Ile Xaa Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30

aaa aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg 144  
 Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45

tct tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg 192  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60

cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc 240  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80

ctg aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg 288  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95

gat cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct 336  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110

tgc att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg 384  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125

cac cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct 432  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140

ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc 480  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160

cgt gat ctg aaa tac gtt gct gat ggt ray ctg dnn ctg cgt acc tct 528  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Xaa Leu Xaa Leu Arg Thr Ser  
 165 170 175

acc cat ccg gaa tct acc taa 549  
 Thr His Pro Glu Ser Thr \*

<210> 148  
 <211> 182  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Human IL-29 C5 mutant for expression in E. coli

<221> VARIANT  
 <222> (11)...(11)  
 <223> Xaa = Thr or Pro

<221> VARIANT  
 <222> (19)...(19)  
 <223> Xaa = Gly or Asp

<221> VARIANT  
 <222> (170)...(170)  
 <223> Xaa = Asp or Asn

<221> VARIANT  
 <222> (172)...(172)  
 <223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 148  
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Xaa Thr Gly Lys Gly Cys  
 1 5 10 15  
 His Ile Xaa Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe  
 20 25 30  
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp  
 35 40 45  
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu  
 50 55 60  
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr  
 65 70 75 80  
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu  
 85 90 95  
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala  
 100 105 110  
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu  
 115 120 125  
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala  
 130 135 140  
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr  
 145 150 155 160  
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Xaa Leu Xaa Leu Arg Thr Ser  
 165 170 175  
 Thr His Pro Glu Ser Thr  
 180

<210> 149  
 <211> 531  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human IL-29 d2/7 C5 mutant for expression in E.  
 coli

<221> CDS  
 <222> (1)...(531)

<221> variation  
 <222> (497)...(498)  
 <223> n = A, T, G or C

<400> 149  
 atg aaa cca acc acc act ggt aaa ggt tgc cac atc ggt cgt ttc aaa 48  
 Met Lys Pro Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys  
 1 5 10 15  
 tct ctg tct ccg cag gaa ctg gct tct ttc aaa aaa gct cgt gac gct 96

Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala  
 20 25 30

ctg gaa gaa tct ctg aaa ctg aaa aac tgg tct tgc tct tct ccg gtt 144  
 Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val  
 35 40 45

ttc ccg ggt aac tgg gat ctg cgt ctg ctg cag gtt cgt gaa cgt ccg 192  
 Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro  
 50 55 60

ggt gct ctg gaa gct gaa ctg gct ctg acc ctg aaa gtt ctg gaa gct 240  
 Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala  
 65 70 75 80

gct gca ggt cct gct ctg gaa gat gtt ctg gat cag ccg ctg cac act 288  
 Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr  
 85 90 95

ctg cac cac atc ctg tct cag ctg cag gct tgc att caa ccg caa ccg 336  
 Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro  
 100 105 110

acc gct ggt ccg cgt ccg cgt ggt cgt ctg cac cac tgg ctg cat cgt 384  
 Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg  
 115 120 125

ctg cag gaa gct ccg aaa aaa gaa tct gct ggt tgc ctg gaa gct tct 432  
 Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser  
 130 135 140

gtt acc ttc aac ctg ttc cgt ctg ctg acc cgt gat ctg aaa tac gtt 480  
 Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val  
 145 150 155 160

gct gat ggt aac ctg dnn ctg cgt acc tct acc cat ccg gaa tct acc 528  
 Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr  
 165 170 175

taa 531  
 \*

<210> 150  
 <211> 176  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Human IL-29 d2/7 C5 mutant for expression in E.  
 coli

<221> VARIANT  
 <222> (166)...(166)  
 <223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 150  
 Met Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys  
 1 5 10 15  
 Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala  
 20 25 30  
 Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val  
 35 40 45  
 Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro

50		55		60
Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala				
65		70		75
Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr				
	85		90	
Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro				
	100		105	
Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg				
	115		120	
Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser				
	130		135	
Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val				
145		150		155
Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr				
	165		170	
				175

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